MODULATION OF APOLIPOPROTEIN C-III EXPRESSION

FIELD OF THE INVENTION

The present invention provides compositions and methods for modulating the expression of apolipoprotein C-III. In particular, this invention relates to compounds, particularly oligonucleotide compounds, which, in preferred embodiments, hybridize with nucleic acid molecules encoding apolipoprotein C-III. Such compounds are shown herein to modulate the expression of apolipoprotein C-III.

BACKGROUND OF THE INVENTION

Lipoproteins are globular, micelle-like particles that consist of a non-polar core of acylglycerols and cholesteryl esters surrounded by an amphiphilic coating of protein, phospholipid and cholesterol. Lipoproteins have been classified into five broad categories on the basis of their functional and physical properties: chylomicrons, which transport dietary lipids from intestine to tissues; very low density lipoproteins (VLDL); intermediate density lipoproteins (IDL); low density lipoproteins (LDL); all of which transport triacylglycerols and cholesterol from the liver to tissues; and high density lipoproteins (HDL), which transport endogenous cholesterol from tissues to the liver.

Lipoprotein particles undergo continuous metabolic processing and have variable properties and compositions. Lipoprotein densities increase without decreasing particle diameter because the density of their outer coatings is less than that of the inner core. The protein components of lipoproteins are known as apolipoproteins. At least nine apolipoproteins are distributed in significant amounts among the various human lipoproteins.

Apolipoprotein C-III is a constituent of HDL and of triglyceride-rich lipoproteins and has a role in hypertriglyceridemia, a risk factor for coronary artery disease. Apolipoprotein C-III slows this clearance of triglyceride-rich lipoproteins by inhibiting lipolysis, both through inhibition of lipoprotein lipase and by interfering with lipoprotein binding to the cell-surface glycosaminoglycan matrix (Shachter, *Curr. Opin. Lipidol.*, **2001**, *12*, 297-304).

The gene encoding human apolipoprotein C-III (also called APOC3, APOC-III, APO CIII, and APO C-III) was cloned in 1984 by three research groups (Levy-Wilson *et al.*, *DNA*, **1984**, *3*, 359-364; Protter *et al.*, *DNA*, **1984**, *3*, 449-456; Sharpe *et al.*, *Nucleic Acids Res.*, **1984**, *12*, 3917-3932). The coding sequence is interrupted by three introns (Protter *et al.*, *DNA*, **1984**, *3*, 449-456). The human apolipoprotein C-III gene is located approximately 2.6kB to the 3′ direction of the apolipoprotein A-1 gene and these two genes are convergently transcribed (Karathanasis, *Proc. Natl. Acad. Sci. U. S. A.*, **1985**, *82*, 6374-6378). Also cloned was a variant of human apolipoprotein C-III with a Thr74 to Ala74 mutation from a patient with unusually high level of serum apolipoprotein C-III. As the Thr74 is O-glycosylated, the Ala74 mutant therefore resulted in increased levels of serum apolipoprotein C-III lacking the carbohydrate moiety (Maeda *et al.*, *J. Lipid Res.*, **1987**, *28*, 1405-1409).

Five polymorphisms have been identified in the promoter region of the gene: C(-641) to A, G(-630) to A, T(-625) to deletion, C(-482) to T and T(-455) to C). All of these polymorphisms are in linkage disequilibrium with the *Sst*I polymorphism in the 3′ untranslated region. The *Sst*I site distinguishes the S1 and S2 alleles and the S2 allele has

been associated with elevated plasma triglyceride levels (Dammerman *et al.*, *Proc. Natl. Acad. Sci. U. S. A.*, **1993**, *90*, 4562-4566). The apolipoprotein C-III promoter is downregulated by insulin and this polymorphic site abolishes the insulin regulation. Thus the potential overexpression of apolipoprotein C-III resulting from the loss of insulin regulation may be a contributing factor to the development of hypertriglyceridemia associated with the S2 allele (Li *et al.*, *J. Clin. Invest.*, **1995**, *96*, 2601-2605). The T(-455) to C polymorphism has been associated with an increased risk of coronary artery disease (Olivieri *et al.*, *J. Lipid Res.*, **2002**, *43*, 1450-1457).

In addition to insulin, other regulators of apolipoprotein C-III gene expression have been identified. A response element for the nuclear orphan receptor rev-erb alpha has been located at positions -23/-18 in the apolipoprotein C-III promoter region and rev-erb alpha decreases apolipoprotein C-III promoter activity (Raspe *et al.*, *J. Lipid Res.*, **2002**, *43*, 2172-2179). The apolipoprotein C-III promoter region -86 to -74 is recognized by two nuclear factors CIIIb1 and CIIIB2 (Ogami *et al.*, *J. Biol. Chem.*, **1991**, *266*, 9640-9646). Apolipoprotein C-III expression is also upregulated by retinoids acting via the retinoid X receptor, and alterations in retinoid X receptor abundance affects apolipoprotein C-III transcription (Vu-Dac *et al.*, *J. Clin. Invest.*, **1998**, *102*, 625-632). Specificity protein 1 (Sp1) and hepatocyte nuclear factor-4 (HNF-4) have been shown to work synergistically to transactivate the apolipoprotein C-III promoter via the HNF-4 binding site (Kardassis *et al.*, *Biochemistry*, **2002**, *41*, 1217-1228). HNF-4 also works in conjunction with SMAD3-SMAD4 to transactivate the

apolipoprotein C-III promoter (Kardassis *et al.*, *J. Biol. Chem.*, **2000**, *275*, 41405-41414).

Transgenic and knockout mice have further defined the role of apolipoprotein C-III in lipolysis. Overexpression of apolipoprotein C-III in transgenic mice leads to hypertriglyceridemia and impaired clearance of VLDL-triglycerides (de Silva *et al.*, *J. Biol. Chem.*, **1994**, *269*, 2324-2335; Ito *et al.*, *Science*, **1990**, *249*, 790-793). Knockout mice with a total absence of the apolipoprotein C-III protein exhibited significantly reduced plasma cholesterol and triglyceride levels compared with wild-type mice and were protected from postprandial hypertriglyceridemia (Maeda *et al.*, *J. Biol. Chem.*, **1994**, *269*, 23610-23616).

Currently, there are no known therapeutic agents that affect the function of apolipoprotein C-III. The hypolipidemic effect of the fibrate class of drugs has been postulated to occur via a mechanism where peroxisome proliferator activated receptor (PPAR) mediates the displacement of HNF-4 from the apolipoprotein C-III promoter, resulting in transcriptional suppression of apolipoprotein C-III (Hertz *et al.*, *J. Biol. Chem.*, **1995**, *270*, 13470-13475). The statin class of hypolipidemic drugs also lower triglyceride levels via an unknown mechanism, which results in increases in lipoprotein lipase mRNA and a decrease in plasma levels of apolipoprotein C-III (Schoonjans *et al.*, *FEBS Lett.*, **1999**, *452*, 160-164). Consequently, there remains a long felt need for additional agents capable of effectively inhibiting apolipoprotein C-III function.

SUMMARY OF THE INVENTION

The present invention provides compositions and methods for modulating apolipoprotein C-III expression. Antisense technology is emerging as an effective means for reducing the expression of specific gene products and is uniquely useful in a number of therapeutic, diagnostic, and research applications for the modulation of apolipoprotein C-III expression.

The present invention is directed to compounds, especially nucleic acid and nucleic acid-like oligomers, which are targeted to a nucleic acid encoding apolipoprotein C-III, and which modulate the expression of apolipoprotein C-III. Pharmaceutical and other compositions comprising the compounds of the invention are also provided.

Further provided are methods of screening for modulators of apolipoprotein C-III and methods of modulating the expression of apolipoprotein C-III in cells, tissues or animals comprising contacting said cells, tissues or animals with one or more of the compounds or compositions of the invention. In these methods, the cells or tissues are contacted *in vivo*. Alternatively, the cells or tissues are contacted *ex vivo*.

Methods of treating an animal, particularly a human, suspected of having or being prone to a disease or condition associated with expression of apolipoprotein C-III are also set forth herein. Such methods comprise administering a therapeutically or prophylactically effective amount of one or more of the compounds or compositions of the invention to the person in need of treatment.

Also provided is a method of making a compound of the invention comprising specifically hybridizing *in vitro* a

first nucleobase strand comprising a sequence of at least 8 contiguous nucleobases of the sequence set forth in SEQ ID NO: 4 and/or SEQ ID NO: 18 to a second nucleobase strand comprising a sequence sufficiently complementary to said first strand so as to permit stable hybridization.

The invention further provides a compound of the invention for use in therapy.

The invention further provides use of a compound or composition of the invention in the manufacture of a medicament for the treatment of any and all conditions disclosed herein.

DETAILED DESCRIPTION OF THE INVENTION

A. Overview of the Invention

The present invention employs compounds, preferably oligonucleotides and similar species for use in modulating the function or effect of nucleic acid molecules encoding apolipoprotein C-III. This is accomplished by providing oligonucleotides that specifically hybridize with one or more nucleic acid molecules encoding apolipoprotein C-III.

As used herein, the terms "target nucleic acid" and "nucleic acid molecule encoding apolipoprotein C-III" have been used for convenience to include DNA encoding apolipoprotein C-III, RNA (including pre-mRNA and mRNA or portions thereof) transcribed from such DNA, and also cDNA derived from such RNA.

The hybridization of a compound of this invention with its target nucleic acid is generally referred to as "antisense". Consequently, the mechanism included in the practice of some preferred embodiments of the invention is referred to herein as "antisense inhibition." Such antisense inhibition is typically based upon hydrogen

bonding-based hybridization of oligonucleotide strands or segments such that at least one strand or segment is cleaved, degraded, or otherwise rendered inoperable. In this regard, it is presently preferred to target specific nucleic acid molecules and their functions for such antisense inhibition.

The functions of DNA to be interfered with include replication and transcription. Replication and transcription, for example, can be from an endogenous cellular template, a vector, a plasmid construct or otherwise. The functions of RNA to be interfered with can include functions such as translocation of the RNA to a site of protein translation, translocation of the RNA to sites within the cell which are distant from the site of RNA synthesis, translation of protein from the RNA, splicing of the RNA to yield one or more RNA species, and catalytic activity or complex formation involving the RNA which may be engaged in or facilitated by the RNA. One preferred result of such interference with target nucleic acid function is modulation of the expression of apolipoprotein C-III. In the context of the present invention, "modulation" and "modulation of expression" mean either an increase (stimulation) or a decrease (inhibition) in the amount or levels of a nucleic acid molecule encoding the gene, e.g., DNA or RNA. Inhibition is often the preferred form of modulation of expression and mRNA is often a preferred target nucleic acid.

In the context of this invention, "hybridization" means the pairing of complementary strands of oligomeric compounds. In the present invention, the preferred mechanism of pairing involves hydrogen bonding, which may be Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen

bonding, between complementary nucleoside or nucleotide bases (nucleobases) of the strands of oligomeric compounds. For example, adenine and thymine are complementary nucleobases, which pair through the formation of hydrogen bonds. Hybridization can occur under varying circumstances.

An antisense compound is specifically hybridizable when binding of the compound to the target nucleic acid interferes with the normal function of the target nucleic acid to cause a loss of activity, and there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target nucleic acid sequences under conditions in which specific binding is desired, i.e., under physiological conditions in the case of *in vivo* assays or therapeutic treatment, and under conditions in which assays are performed in the case of *in vitro* assays.

In the present invention the phrase "stringent hybridization conditions" or "stringent conditions" refers to conditions under which a compound of the invention will hybridize to its target sequence, but to a minimal number of other sequences. Stringent conditions are sequence-dependent and are different in different circumstances. In the context of this invention, "stringent conditions" under which oligomeric compounds hybridize to a target sequence are determined by the nature and composition of the oligomeric compounds and the assays in which they are being investigated.

"Complementary," as used herein, refers to the capacity for precise pairing between two nucleobases of an oligomeric compound. For example, if a nucleobase at a certain position of an oligonucleotide (an oligomeric compound), is capable of hydrogen bonding with a nucleobase at a certain position of a target nucleic acid, said target nucleic acid

being a DNA, RNA, or oligonucleotide molecule, then the position of hydrogen bonding between the oligonucleotide and the target nucleic acid is considered to be a complementary position. The oligonucleotide and the further DNA, RNA, or oligonucleotide molecule are complementary to each other when a sufficient number of complementary positions in each molecule are occupied by nucleobases that can hydrogen bond with each other. Thus, "specifically hybridizable" and "complementary" are terms that are used to indicate a sufficient degree of precise pairing or complementarity over a sufficient number of nucleobases such that stable and specific binding occurs between the oligonucleotide and a target nucleic acid.

It is understood in the art that the sequence of the antisense compound of this invention can be, but need not be, 100% complementary to that of the target nucleic acid to be specifically hybridizable. Moreover, an oligonucleotide may hybridize over one or more segments such that intervening or adjacent segments are not involved in the hybridization event (e.g., a loop structure or hairpin structure). In one embodiment, the antisense compounds of the present invention comprise at least 70%, or at least 75%, or at least 80%, or at least 85% sequence complementarity to a target region within the target nucleic acid. In another embodiment, the antisense compounds of this invention comprise 90% sequence complementarity and even more preferably comprise 95% or at least 99% sequence complementarity to the target region within the target nucleic acid sequence to which they are targeted. Preferably, the antisense compounds comprise at least 8 contiguous nucleobases of an antisense compound disclosed herein. For example, an antisense compound in which 18 of

20 nucleobases of the antisense compound are complementary to a target region, and would therefore specifically hybridize, would represent 90 percent complementarity. In this example, the remaining noncomplementary nucleobases may be clustered or interspersed with complementary nucleobases and need not be contiguous to each other or to complementary nucleobases. As such, an antisense compound which is 18 nucleobases in length having 4 (four) noncomplementary nucleobases which are flanked by two regions of complete complementarity with the target nucleic acid would have 77.8% overall complementarity with the target nucleic acid and would thus fall within the scope of the present invention. Percent complementarity of an antisense compound with a region of a target nucleic acid can be determined routinely using BLAST programs (basic local alignment search tools) and PowerBLAST programs known in the art (Altschul *et al.*, *J. Mol. Biol.*, **1990**, 215, 403-410; Zhang and Madden, *Genome Res.*, **1997**, 7, 649-656).

Percent homology, sequence identity or complementarity, can be determined by, for example, the Gap program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, Madison WI), using default settings, which uses the algorithm of Smith and Waterman (*Adv. Appl. Math.*, **1981**, 2, 482-489). In some preferred embodiments, homology, sequence identity or complementarity, between the oligomeric and target is between about 50% to about 60%. In some embodiments, homology, sequence identity or complementarity, is between about 60% and about 70%. In preferred embodiments, homology, sequence identity or complementarity, is between about 70% and about 80%. In more preferred embodiments, homology, sequence identity or complementarity, is between

about 80% and about 90%. In some preferred embodiments, homology, sequence identity or complementarity, is about 90%, about 92%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99%.

B. Compounds of the Invention

According to the present invention, compounds include antisense oligomeric compounds, antisense oligonucleotides, ribozymes, external guide sequence (EGS) oligonucleotides, alternate splicers, primers, probes, and other oligomeric compounds that hybridize to at least a portion of the target nucleic acid. As such, these compounds may be introduced in the form of single-stranded, double-stranded, circular or hairpin oligomeric compounds and may contain structural elements such as internal or terminal bulges or loops. Once introduced to a system, the compounds of the invention may elicit the action of one or more enzymes or structural proteins to effect modification of the target nucleic acid.

One non-limiting example of such an enzyme is RNAse H, a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. It is known in the art that single-stranded antisense compounds which are "DNA-like" elicit RNAse H. Activation of RNAse H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide-mediated inhibition of gene expression. Similar roles have been postulated for other ribonucleases such as those in the RNAse III and ribonuclease L family of enzymes.

While the preferred form of antisense compound is a single-stranded antisense oligonucleotide, in many species the introduction of double-stranded structures, such as double-stranded RNA (dsRNA) molecules, induces potent and

specific antisense-mediated reduction of the function of a gene or its associated gene products. This phenomenon occurs in both plants and animals and is believed to have an evolutionary connection to viral defense and transposon silencing.

The first evidence that dsRNA could lead to gene silencing in animals came in 1995 from work in the nematode, *Caenorhabditis elegans* (Guo and Kempheus, *Cell*, **1995**, 81, 611-620). The primary interference effects of dsRNA are posttranscriptional (Montgomery *et al.*, *Proc. Natl. Acad. Sci. USA*, **1998**, *95*, 15502-15507). The posttranscriptional antisense mechanism defined in *Caenorhabditis elegans* resulting from exposure to double-stranded RNA (dsRNA) has since been designated RNA interference (RNAi). This term has been generalized to mean antisense-mediated gene silencing involving the introduction of dsRNA leading to the sequence-specific reduction of endogenous targeted mRNA levels (Fire *et al.*, *Nature*, **1998**, 391, 806-811). Recently, the single-stranded RNA oligomers of antisense polarity of the dsRNAs have been reported to be potent inducers of RNAi (Tijsterman *et al.*, *Science*, **2002**, *295*, 694-697).

In the context of this invention, the term "oligomeric compound" refers to a polymer or oligomer comprising a plurality of monomeric units. In the context of this invention, the term "oligonucleotide" refers to an oligomer or polymer of ribonucleic acid (RNA) or deoxyribonucleic acid (DNA) or mimetics, chimeras, analogs and homologs thereof. This term includes oligonucleotides composed of naturally occurring nucleobases, sugars and covalent internucleoside (backbone) linkages as well as oligonucleotides having non-naturally occurring portions which function similarly. Such modified or substituted

oligonucleotides are often preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for a target nucleic acid and increased stability in the presence of nucleases.

The oligonucleotides of the present invention also include modified oligonucleotides in which a different nucleobase is present at one or more of the nucleotide positions in the oligonucleotide. For example, if the first nucleotide is adenosine, modified oligonucleotides may be produced that contain thymidine, guanosine or cytidine at this position. This may be done at any of the positions of the oligonucleotide. These oligonucleotides are then tested using the methods described herein to determine their ability to inhibit expression of apolipoprotein C-III.

While oligonucleotides are a preferred form of the compounds of this invention, the present invention comprehends other families of compounds as well, including but not limited to oligonucleotide analogs and mimetics such as those described herein.

The compounds in accordance with this invention preferably comprise from about 8 to about 80 nucleobases (i.e. from about 8 to about 80 linked nucleosides). One of ordinary skill in the art will appreciate that the invention embodies compounds of 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, or 80 nucleobases in length.

In one preferred embodiment, the compounds of the invention are 12 to 50 nucleobases in length. One having

ordinary skill in the art will appreciate that this embodies compounds of 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleobases in length.

In another preferred embodiment, the compounds of the invention are 15 to 30 nucleobases in length. One having ordinary skill in the art will appreciate that this embodies compounds of 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleobases in length.

Particularly preferred compounds are oligonucleotides from about 12 to about 50 nucleobases, even more preferably those comprising from about 15 to about 30 nucleobases.

Antisense compounds 8-80 nucleobases in length comprising a stretch of at least eight (8) consecutive nucleobases selected from within the illustrative antisense compounds are considered to be suitable antisense compounds as well.

Exemplary preferred antisense compounds include oligonucleotide sequences that comprise at least the 8 consecutive nucleobases from the 5'-terminus of one of the illustrative preferred antisense compounds (the remaining nucleobases being a consecutive stretch of the same oligonucleotide beginning immediately upstream of the 5'-terminus of the antisense compound which is specifically hybridizable to the target nucleic acid and continuing until the oligonucleotide contains about 8 to about 80 nucleobases). Similarly preferred antisense compounds are represented by oligonucleotide sequences that comprise at least the 8 consecutive nucleobases from the 3'-terminus of one of the illustrative preferred antisense compounds (the remaining nucleobases being a consecutive stretch of the

same oligonucleotide beginning immediately downstream of the 3'-terminus of the antisense compound which is specifically hybridizable to the target nucleic acid and continuing until the oligonucleotide contains about 8 to about 80 nucleobases). Exemplary compounds of this invention from a variety of mammalian sources, including human, may be found identified in the Examples and listed in Tables 1 through 21. One having skill in the art armed with the preferred antisense compounds illustrated herein will be able, without undue experimentation, to identify further preferred antisense compounds.

C. Targets of the Invention

"Targeting" an antisense compound to a target nucleic acid molecule encoding apolipoprotein C-III, in the context of this invention, can be a multi-step process. The process usually begins with the identification of a target nucleic acid whose function is to be modulated. This target nucleic acid may be, for example, a cellular gene (or mRNA transcribed from the gene) whose expression is associated with a particular disorder or disease state, or a nucleic acid molecule from an infectious agent. In the present invention, the target nucleic acid encodes apolipoprotein C-III.

The targeting process usually also includes determination of at least one target region, segment, or site within the target nucleic acid for the antisense interaction to occur such that the desired effect, e.g., modulation of expression, will result. Within the context of the present invention, the term "region" is defined as a portion of the target nucleic acid having at least one identifiable structure, function, or characteristic. Within

regions of target nucleic acids are segments. "Segments" are defined as smaller or sub-portions of regions within a target nucleic acid. "Sites," as used in the present invention, are defined as positions within a target nucleic acid.

Since, as is known in the art, the translation initiation codon is typically 5'-AUG (in transcribed mRNA molecules; 5'-ATG in the corresponding DNA molecule), the translation initiation codon is also referred to as the "AUG codon," the "start codon" or the "AUG start codon". A minority of genes, having translation initiation codons with the RNA sequence 5'-GUG, 5'-UUG or 5'-CUG, and 5'-AUA, 5'-ACG and 5'-CUG, have been shown to function *in vivo*. Thus, the terms "translation initiation codon" and "start codon" can encompass many codon sequences, even though the initiator amino acid in each instance is typically methionine (in eukaryotes) or formylmethionine (in prokaryotes). It is also known in the art that eukaryotic and prokaryotic genes may have two or more alternative start codons, any one of which may be preferentially utilized for translation initiation in a particular cell type or tissue, or under a particular set of conditions. In the context of the invention, "start codon" and "translation initiation codon" refer to the codon or codons that are used *in vivo* to initiate translation of an mRNA transcribed from a gene encoding apolipoprotein C-III, regardless of the sequence(s) of such codons. It is also known in the art that a translation termination codon (or "stop codon") of a gene may have one of three sequences, i.e., 5'-UAA, 5'-UAG and 5'-UGA (the corresponding DNA sequences are 5'-TAA, 5'-TAG and 5'-TGA, respectively).

The terms "start codon region" and "translation initiation codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation codon. Similarly, the terms "stop codon region" and "translation termination codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation termination codon. Consequently, the "start codon region" (or "translation initiation codon region") and the "stop codon region" (or "translation termination codon region") are all regions that may be targeted effectively with the antisense compounds of the present invention.

The open reading frame (ORF) or "coding region," which is known in the art to refer to the region between the translation initiation codon and the translation termination codon, is also a region which may be targeted effectively. Within the context of the present invention, a preferred region is the intragenic region encompassing the translation initiation or termination codon of the open reading frame (ORF) of a gene.

Other target regions include the 5' untranslated region (5'UTR), known in the art to refer to the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA (or corresponding nucleotides on the gene), and the 3' untranslated region (3'UTR), known in the art to refer to the portion of an mRNA in the 3' direction from the translation termination codon, and thus including nucleotides between the translation termination codon and 3'

end of an mRNA (or corresponding nucleotides on the gene). The 5' cap site of an mRNA comprises an N7-methylated guanosine residue joined to the 5'-most residue of the mRNA via a 5'-5' triphosphate linkage. The 5' cap region of an mRNA is considered to include the 5' cap structure itself as well as the first 50 nucleotides adjacent to the cap site. It is also preferred to target the 5' cap region.

Accordingly, the present invention provides antisense compounds that target a portion of nucleobases 1 - 533 as set forth in SEQ ID NO: 18. In one embodiment, the antisense compounds target at least an 8 nucleobase portion of nucleobases 1 - 533 as set forth in SEQ ID NO: 18 and Tables 1 and 4. In another embodiment, the antisense compounds target at least an 8 nucleobase portion of nucleobases comprising the 5' UTR as set forth in SEQ ID NO: 18 and Tables 1 and 4. In another embodiment, the antisense compounds target at least an 8 nucleobase portion of nucleobases comprising the 3' UTR as set forth in SEQ ID NO: 18 and Tables 1 and 4. In another embodiment, the antisense compounds target at least an 8 nucleobase portion of nucleobases comprising the coding region as set forth in SEQ ID NO: 18 and Tables 1 and 4. In still other embodiments, the antisense compounds target at least an 8 nucleobase portion of a "preferred target segment" (as defined herein) as set forth in Table 3.

Further, the present invention provides antisense compounds that target a portion of nucleobases 1 - 3958 as set forth in SEQ ID NO: 4. In one embodiment, the antisense compounds target at least an 8 nucleobase portion of nucleobases 1 - 3958 as set forth in SEQ ID NO: 4 and Tables 1 and 4. In another embodiment, the antisense compounds target at least an 8 nucleobase portion of nucleobases

comprising the 5' UTR as set forth in SEQ ID NO: 4 and Tables 1 and 4. In another embodiment, the antisense compounds target at least an 8 nucleobase portion of nucleobases comprising the 3' UTR as set forth in SEQ ID NO: 4 and Tables 1 and 4. In another embodiment, the antisense compounds target at least an 8 nucleobase portion of nucleobases comprising the coding region as set forth in SEQ ID NO: 4 and Tables 1 and 4. In still other embodiments, the antisense compounds target at least an 8 nucleobase portion of a "preferred target segment" (as defined herein) as set forth in Table 3.

Although some eukaryotic mRNA transcripts are directly translated, many contain one or more regions, known as "introns," which are excised from a transcript before it is translated. The remaining (and therefore translated) regions are known as "exons" and are spliced together to form a continuous mRNA sequence. Targeting splice sites, i.e., intron-exon junctions or exon-intron junctions, may also be particularly useful in situations where aberrant splicing is implicated in disease, or where an overproduction of a particular splice product is implicated in disease. Aberrant fusion junctions due to rearrangements or deletions are also preferred target sites. mRNA transcripts produced via the process of splicing of two (or more) mRNAs from different gene sources are known as "fusion transcripts". It is also known that introns can be effectively targeted using antisense compounds targeted to, for example, DNA or pre-mRNA.

Alternative RNA transcripts can be produced from the same genomic region of DNA. These alternative transcripts are generally known as "variants". More specifically, "pre-mRNA variants" are transcripts produced from the same

genomic DNA that differ from other transcripts produced from the same genomic DNA in either their start or stop position and contain both intronic and exonic sequence.

Upon excision of one or more exon or intron regions, or portions thereof during splicing, pre-mRNA variants produce smaller "mRNA variants". Consequently, mRNA variants are processed pre-mRNA variants and each unique pre-mRNA variant must always produce a unique mRNA variant as a result of splicing. These mRNA variants are also known as "alternative splice variants". If no splicing of the pre-mRNA variant occurs then the pre-mRNA variant is identical to the mRNA variant.

Variants can be produced through the use of alternative signals to start or stop transcription. Pre-mRNAs and mRNAs can possess more than one start codon or stop codon. Variants that originate from a pre-mRNA or mRNA that use alternative start codons are known as "alternative start variants" of that pre-mRNA or mRNA. Those transcripts that use an alternative stop codon are known as "alternative stop variants" of that pre-mRNA or mRNA. One specific type of alternative stop variant is the "polyA variant" in which the multiple transcripts produced result from the alternative selection of one of the "polyA stop signals" by the transcription machinery, thereby producing transcripts that terminate at unique polyA sites. Within the context of the invention, the types of variants described herein are also preferred target nucleic acids.

The locations on the target nucleic acid to which the preferred antisense compounds hybridize are hereinbelow referred to as "preferred target segments." As used herein the term "preferred target segment" is defined as at least an 8-nucleobase portion of a target region to which an

active antisense compound is targeted. While not wishing to be bound by theory, it is presently believed that these target segments represent portions of the target nucleic acid that are accessible for hybridization.

While the specific sequences of certain preferred target segments are set forth herein, one of skill in the art will recognize that these serve to illustrate and describe particular embodiments within the scope of the present invention. Additional preferred target segments may be identified by one having ordinary skill.

Target segments 8-80 nucleobases in length comprising a stretch of at least eight (8) consecutive nucleobases selected from within the illustrative preferred target segments are considered to be suitable for targeting as well.

Target segments can include DNA or RNA sequences that comprise at least the 8 consecutive nucleobases from the 5'-terminus of one of the illustrative preferred target segments (the remaining nucleobases being a consecutive stretch of the same DNA or RNA beginning immediately upstream of the 5'-terminus of the target segment and continuing until the DNA or RNA contains about 8 to about 80 nucleobases). Similarly preferred target segments are represented by DNA or RNA sequences that comprise at least the 8 consecutive nucleobases from the 3'-terminus of one of the illustrative preferred target segments (the remaining nucleobases being a consecutive stretch of the same DNA or RNA beginning immediately downstream of the 3'-terminus of the target segment and continuing until the DNA or RNA contains about 8 to about 80 nucleobases). One having skill in the art armed with the preferred target segments illustrated herein will be able, without undue

experimentation, to identify further preferred target segments.

Once one or more target regions, segments or sites have been identified, antisense compounds are chosen which are sufficiently complementary to the target, i.e., hybridize sufficiently well and with sufficient specificity, to give the desired effect.

The oligomeric compounds are targeted to or not targeted to regions of the target apolipoprotein C-III nucleobase sequence (e.g., such as those disclosed in Examples 15 and 17) comprising nucleobases 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 601-650, 651-700, 701-750, 751-800, 801-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2591-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, 3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-3950, 3951-3958 of SEQ ID NO: 4, or any combination thereof.

Further, the oligomeric compounds are targeted to or not targeted to regions of the target apolipoprotein C-III nucleobase sequence (e.g., such as those disclosed in Examples 15 and 17) comprising nucleobases 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-

450, 451-500, 501-533 of SEQ ID NO: 18, or any combination thereof.

In one embodiment, the oligonucleotide compounds of this invention are 100% complementary to these sequences or to small sequences found within each of the above-listed sequences. Preferably, the antisense compounds comprise at least 8 contiguous nucleobases of an antisense compound disclosed herein. In another embodiment, the oligonucleotide compounds have from at least 3 or 5 mismatches per 20 consecutive nucleobases in individual nucleobase positions to these target regions. Still other compounds of the invention are targeted to overlapping regions of the above-identified portions of the apolipoprotein C-III sequence.

D. Screening and Target Validation

In a further embodiment, the "preferred target segments" identified herein may be employed in a screen for additional compounds that modulate the expression of apolipoprotein C-III. "Modulators" are those compounds that decrease or increase the expression of a nucleic acid molecule encoding apolipoprotein C-III and which comprise at least an 8-nucleobase portion that is complementary to a preferred target segment. The screening method comprises the steps of contacting a preferred target segment of a nucleic acid molecule encoding apolipoprotein C-III with one or more candidate modulators, and selecting for one or more candidate modulators which decrease or increase the expression of a nucleic acid molecule encoding apolipoprotein C-III. Once it is shown that the candidate modulator or modulators are capable of modulating (e.g. either decreasing or increasing) the expression of a nucleic

acid molecule encoding apolipoprotein C-III, the modulator may then be employed in further investigative studies of the function of apolipoprotein C-III, or for use as a research, diagnostic, or therapeutic agent in accordance with the present invention.

The preferred target segments of the present invention may be also be combined with their respective complementary antisense compounds of the present invention to form stabilized double-stranded (duplexed) oligonucleotides.

Such double stranded oligonucleotide moieties have been shown in the art to modulate target expression and regulate translation as well as RNA processing via an antisense mechanism. Moreover, the double-stranded moieties may be subject to chemical modifications (Fire *et al.*, *Nature*, **1998**, *391*, 806-811; Timmons and Fire, *Nature* **1998**, *395*, 854; Timmons *et al.*, *Gene*, **2001**, *263*, 103-112; Tabara *et al.*, *Science*, **1998**, 282, 430-431; Montgomery *et al.*, *Proc. Natl. Acad. Sci. USA*, **1998**, *95*, 15502-15507; Tuschl *et al.*, *Genes Dev.*, **1999**, *13*, 3191-3197; Elbashir *et al.*, *Nature*, **2001**, *411*, 494-498; Elbashir *et al.*, *Genes Dev.* **2001**, *15*, 188-200). For example, such double-stranded moieties have been shown to inhibit the target by the classical hybridization of antisense strand of the duplex to the target, thereby triggering enzymatic degradation of the target (Tijsterman *et al.*, *Science*, **2002**, *295*, 694-697).

The compounds of the present invention can also be applied in the areas of drug discovery and target validation. The present invention comprehends the use of the compounds and preferred target segments identified herein in drug discovery efforts to elucidate relationships that exist between apolipoprotein C-III and a disease state, phenotype, or condition. These methods include detecting or modulating

apolipoprotein C-III comprising contacting a sample, tissue, cell, or organism with the compounds of the present invention, measuring the nucleic acid or protein level of apolipoprotein C-III and/or a related phenotypic or chemical endpoint at some time after treatment, and optionally comparing the measured value to a non-treated sample or sample treated with a further compound of the invention. These methods can also be performed in parallel or in combination with other experiments to determine the function of unknown genes for the process of target validation or to determine the validity of a particular gene product as a target for treatment or prevention of a particular disease, condition, or phenotype.

E. Kits, Research Reagents, Diagnostics, and Therapeutics

The compounds of the present invention are utilized for diagnostics, therapeutics, prophylaxis, and as research reagents and kits. In one embodiment, such compounds of the invention are useful in areas of obesity and metabolic-related disorders such as hyperlipidemia. Furthermore, antisense oligonucleotides, which are able to inhibit gene expression with exquisite specificity, are often used by those of ordinary skill to elucidate the function of particular genes or to distinguish between functions of various members of a biological pathway.

For use in kits and diagnostics, the compounds of the present invention, either alone or in combination with other compounds or therapeutics, are used as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion or the entire complement of genes expressed within cells and tissues.

As used herein, the term "system" is defined as any organism, cell, cell culture or tissue that expresses, or is made competent to express products of the gene encoding apolipoprotein C-III. These include, but are not limited to, humans, transgenic animals, cells, cell cultures, tissues, xenografts, transplants and combinations thereof.

As one nonlimiting example, expression patterns within cells or tissues treated with one or more antisense compounds are compared to control cells or tissues not treated with antisense compounds and the patterns produced are analyzed for differential levels of gene expression as they pertain, for example, to disease association, signaling pathway, cellular localization, expression level, size, structure or function of the genes examined. These analyses can be performed on stimulated or unstimulated cells and in the presence or absence of other compounds that affect expression patterns.

Examples of methods of gene expression analysis known in the art include DNA arrays or microarrays (Brazma and Vilo, *FEBS Lett.*, **2000**, 480, 17-24; Celis, *et al.*, *FEBS Lett.*, **2000**, 480, 2-16), SAGE (serial analysis of gene expression)(Madden, *et al.*, *Drug Discov. Today*, **2000**, 5, 415-425), READS (restriction enzyme amplification of digested cDNAs) (Prashar and Weissman, *Methods Enzymol.*, **1999**, 303, 258-72), TOGA (total gene expression analysis) (Sutcliffe, *et al.*, *Proc. Natl. Acad. Sci. U. S. A.*, **2000**, 97, 1976-81), protein arrays and proteomics (Celis, *et al.*, *FEBS Lett.*, **2000**, 480, 2-16; Jungblut, *et al.*, *Electrophoresis*, **1999**, 20, 2100-10), expressed sequence tag (EST) sequencing (Celis, *et al.*, *FEBS Lett.*, **2000**, 480, 2-16; Larsson, *et al.*, *J. Biotechnol.*, **2000**, 80, 143-57), subtractive RNA fingerprinting (SuRF) (Fuchs, *et al.*, *Anal.*

Biochem., **2000**, 286, 91-98; Larson, *et al.*, *Cytometry*, **2000**, 41, 203-208), subtractive cloning, differential display (DD) (Jurecic and Belmont, *Curr. Opin. Microbiol.*, **2000**, 3, 316-21), comparative genomic hybridization (Carulli, *et al.*, *J. Cell Biochem. Suppl.*, **1998**, 31, 286-96), FISH (fluorescent *in situ* hybridization) techniques (Going and Gusterson, *Eur. J. Cancer*, **1999**, 35, 1895-904) and mass spectrometry methods (To, *Comb. Chem. High Throughput Screen*, **2000**, 3, 235-41).

The compounds of the invention are useful for research and diagnostics, because these compounds hybridize to nucleic acids encoding apolipoprotein C-III. For example, oligonucleotides that are shown to hybridize with such efficiency and under such conditions as disclosed herein as to be effective apolipoprotein C-III inhibitors will also be effective primers or probes under conditions favoring gene amplification or detection, respectively. These primers and probes are useful in methods requiring the specific detection of nucleic acid molecules encoding apolipoprotein C-III and in the amplification of said nucleic acid molecules for detection or for use in further studies of apolipoprotein C-III. Hybridization of the antisense oligonucleotides, particularly the primers and probes, of the invention with a nucleic acid encoding apolipoprotein C-III can be detected by means known in the art. Such means may include conjugation of an enzyme to the oligonucleotide, radiolabelling of the oligonucleotide or any other suitable detection means. Kits using such detection means for detecting the level of apolipoprotein C-III in a sample may also be prepared.

Also provided is a method of making a compound of the invention comprising specifically hybridizing *in vitro* a first nucleobase strand comprising a sequence of at least 8

contiguous nucleobases of the sequence set forth in SEQ ID NO: 4 and/or SEQ ID NO: 18 to a second nucleobase strand comprising a sequence sufficiently complementary to said first strand so as to permit stable hybridization.

The invention further provides a compound of the invention for use in therapy.

The invention further provides use of a compound or composition of the invention in the manufacture of a medicament for the treatment of any and all conditions disclosed herein.

Among diagnostic uses is the measurement of apolipoprotein C-III in patients to identify those who may benefit from a treatment strategy aimed at reducing levels of apolipoprotein C-III. Such patients suitable for diagnosis include patients with hypertriglyceridemia (e.g., to diagnose tendencies for coronary artery disease), abnormal lipid metabolism, obesity, hyperlipidemia, among other disorders.

The specificity and sensitivity of antisense are also harnessed by those of skill in the art for therapeutic uses. Antisense compounds have been employed as therapeutic moieties in the treatment of disease states in animals, including humans. Antisense oligonucleotide drugs, including ribozymes, have been safely and effectively administered to humans and numerous clinical trials are presently underway. It is thus established that antisense compounds can be useful therapeutic modalities that can be configured to be useful in treatment regimes for the treatment of cells, tissues and animals, especially humans.

For therapeutics, an animal, preferably a human, suspected of having a disease or disorder which can be treated by modulating the expression of apolipoprotein C-III

is treated by administering antisense compounds in accordance with this invention. For example, in one non-limiting embodiment, the methods comprise the step of administering to the animal in need of treatment, a therapeutically effective amount of an apolipoprotein C-III inhibitor. The apolipoprotein C-III inhibitors of the present invention effectively inhibit the activity of the apolipoprotein C-III protein or inhibit the expression of the apolipoprotein C-III protein. For example, such a compound that reduces levels of apolipoprotein C-III is useful to prevent morbidity and mortality for subjects with cardiac-related disorders. For example, as demonstrated in the examples, reduction in apolipoprotein C-III can result in a reduction in the serum levels of cholesterol, triglycerides, and glucose. Thus, apolipoprotein C-III inhibitors are useful in the treatment of hypertriglyceridemia, abnormal lipid metabolism, abnormal cholesterol metabolism, atherosclerosis, hyperlipidemia, diabetes, including Type 2 diabetes, obesity, cardiovascular disease, coronary artery disease, among other disorders relating to abnormal metabolism or otherwise.

In one embodiment, the activity or expression of apolipoprotein C-III in an animal is inhibited by about 10%. Preferably, the activity or expression of apolipoprotein C-III in an animal is inhibited by about 30%. More preferably, the activity or expression of apolipoprotein C-III in an animal is inhibited by 50% or more. Thus, the oligomeric compounds modulate expression of apolipoprotein C-III mRNA by at least 10%, by at least 20%, by at least 25%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, by at least 75%, by at least

80%, by at least 85%, by at least 90%, by at least 95%, by at least 98%, by at least 99%, or by 100%.

For example, the reduction of the expression of apolipoprotein C-III may be measured in serum, adipose tissue, liver or any other body fluid, tissue or organ of the animal. Preferably, the cells contained within said fluids, tissues or organs being analyzed contain a nucleic acid molecule encoding apolipoprotein C-III and/or apolipoprotein C-III.

The compounds of the invention can be utilized in pharmaceutical compositions by adding an effective amount of a compound to a suitable pharmaceutically acceptable diluent or carrier. Use of the compounds and methods of the invention may also be useful prophylactically.

F. Modifications

As is known in the art, a nucleoside is a base-sugar combination. The base portion of the nucleoside is normally a heterocyclic base. The two most common classes of such heterocyclic bases are the purines and the pyrimidines. Nucleotides are nucleosides that further include a phosphate group covalently linked to the sugar portion of the nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to either the 2′, 3′ or 5′ hydroxyl moiety of the sugar. In forming oligonucleotides, the phosphate groups covalently link adjacent nucleosides to one another to form a linear polymeric compound. In turn, the respective ends of this linear polymeric compound can be further joined to form a circular compound, however, linear compounds are generally preferred. In addition, linear compounds may have internal nucleobase complementarity and may therefore fold in a

manner as to produce a fully or partially double-stranded compound. Within oligonucleotides, the phosphate groups are commonly referred to as forming the internucleoside backbone of the oligonucleotide. The normal linkage or backbone of RNA and DNA is a 3′ to 5′ phosphodiester linkage.

Modified Internucleoside Linkages (Backbones)

Specific examples of preferred antisense compounds useful in this invention include oligonucleotides containing modified backbones or non-natural internucleoside linkages. As defined in this specification, oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides.

Preferred modified oligonucleotide backbones containing a phosphorus atom therein include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3′-alkylene phosphonates, 5'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3′-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, selenophosphates and boranophosphates having normal 3′-5′ linkages, 2′-5′ linked analogs of these, and those having inverted polarity wherein one or more internucleotide linkages is a 3' to 3', 5' to 5' or 2' to 2' linkage. Preferred oligonucleotides having

inverted polarity comprise a single 3' to 3' linkage at the 3'-most internucleotide linkage i.e. a single inverted nucleoside residue, which may be abasic (the nucleobase is missing or has a hydroxyl group in place thereof). Various salts, mixed salts and free acid forms are also included.

Representative United States patents that teach the preparation of the above phosphorus-containing linkages include, but are not limited to, U.S. Patent Nos.: 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; 5,194,599; 5,565,555; 5,527,899; 5,721,218; 5,672,697 and 5,625,050, certain of which are commonly owned with this application, and each of which is herein incorporated by reference.

Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; riboacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH_2 component parts.

Representative United States patents that teach the preparation of the above oligonucleosides include, but are not limited to, U.S. Patent Nos.: 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; 5,792,608; 5,646,269 and 5,677,439, certain of which are commonly owned with this application, and each of which is herein incorporated by reference.

Modified sugar and internucleoside linkages-Mimetics

In other preferred oligonucleotide mimetics, both the sugar and the internucleoside linkage (i.e. the backbone), of the nucleotide units are replaced with novel groups. The nucleobase units are maintained for hybridization with an appropriate target nucleic acid. One such compound, an oligonucleotide mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S. Patent Nos.: 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found in Nielsen *et al.*, *Science*, **1991**, 254, 1497-1500.

Preferred embodiments of the invention are oligonucleotides with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular $-CH_2-NH-O-CH_2-$, $-CH_2-N(CH_3)-O-CH_2-$ [known as a methylene (methylimino) or MMI backbone], $-CH_2-O-N(CH_3)-CH_2-$, $-CH_2-N(CH_3)-N(CH_3)-CH_2-$ and $-O-N(CH_3)-CH_2-CH_2-$ [wherein the native phosphodiester backbone is represented as $-O-P-O-CH_2-$] of the above referenced U.S. Patent No. 5,489,677, and the amide backbones of the above referenced U.S. Patent No. 5,602,240. Also preferred are oligonucleotides having morpholino backbone structures of the above-referenced U.S. Patent No. 5,034,506.

Modified sugars

Modified oligonucleotides may also contain one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Particularly preferred are $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3]_2$, where n and m are from 1 to about 10. Other preferred oligonucleotides comprise one of the following at the 2′ position: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkenyl, alkynyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, CF_3, OCF_3, $SOCH_3$, SO_2CH_3, ONO_2, NO_2, N_3, NH_2, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving

the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy (2'-O-$CH_2CH_2OCH_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin *et al.*, *Helv. Chim. Acta*, **1995**, *78*, 486-504) i.e., an alkoxyalkoxy group. A further preferred modification includes 2'-dimethylaminooxyethoxy, i.e., a $O(CH_2)_2ON(CH_3)_2$ group, also known as 2'-DMAOE, as described in examples hereinbelow, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethyl-amino-ethoxy-ethyl or 2'-DMAEOE), i.e., 2'-O-CH_2-O-CH_2-$N(CH_3)_2$, also described in examples hereinbelow.

Other preferred modifications include 2'-methoxy (2'-O-CH_3), 2'-aminopropoxy (2'-$OCH_2CH_2CH_2NH_2$), 2'-allyl (2'-CH_2-$CH=CH_2$), 2'-O-allyl (2'-O-CH_2-$CH=CH_2$) and 2'-fluoro (2'-F). The 2'-modification may be in the arabino (up) position or ribo (down) position. A preferred 2'-arabino modification is 2'-F. Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative United States patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. Patent Nos.: 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; 5,792,747; and 5,700,920, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference in its entirety.

A further preferred modification of the sugar includes Locked Nucleic Acids (LNAs) in which the 2'-hydroxyl group is linked to the 3' or 4' carbon atom of the sugar ring, thereby forming a bicyclic sugar moiety. The linkage is preferably a methylene $(-CH_2-)_n$ group bridging the 2' oxygen atom and the 4' carbon atom wherein n is 1 or 2. LNAs and preparation thereof are described in International Patent Publication Nos. WO 98/39352 and WO 99/14226.

Natural and Modified Nucleobases

Oligonucleotides may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl ($-C\equiv C-CH_3$) uracil and cytosine and other alkynyl derivatives of pyrimidine bases, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 2-F-adenine, 2-amino-adenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further modified nucleobases include tricyclic pyrimidines

such as phenoxazine cytidine(1H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), phenothiazine cytidine (1H-pyrimido[5,4-b][1,4]benzothiazin-2(3H)-one), G-clamps such as a substituted phenoxazine cytidine (e.g. 9-(2-aminoethoxy)-H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), carbazole cytidine (2H-pyrimido[4,5-b]indol-2-one), pyridoindole cytidine (H-pyrido[3',2':4,5]pyrrolo[2,3-d]pyrimidin-2-one). Modified nucleobases may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in United States Patent No. 3,687,808, those disclosed in *The Concise Encyclopedia Of Polymer Science And Engineering*, pages 858-859, Kroschwitz, J.I., ed. John Wiley & Sons, **1990**, those disclosed by Englisch *et al.*, *Angewandte Chemie*, International Edition, **1991**, *30*, 613, and those disclosed by Sanghvi, Y.S., Chapter 15, *Antisense Research and Applications*, pages 289-302, Crooke, S.T. and Lebleu, B. , ed., CRC Press, **1993**. Certain of these nucleobases are particularly useful for increasing the binding affinity of the compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2 °C and are presently preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

Representative United States patents that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include,

but are not limited to, the above noted U.S. Patent No. 3,687,808, as well as U.S. Patent Nos.: 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; 5,645,985; 5,830,653; 5,763,588; 6,005,096; and 5,681,941, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference, and U.S. Patent No. 5,750,692, which is commonly owned with the instant application and also herein incorporated by reference.

Conjugates

Another modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. These moieties or conjugates can include conjugate groups covalently bound to functional groups such as primary or secondary hydroxyl groups. Conjugate groups of the invention include intercalators, reporter molecules, polyamines, polyamides, polyethylene glycols, polyethers, groups that enhance the pharmacodynamic properties of oligomers, and groups that enhance the pharmacokinetic properties of oligomers. Typical conjugate groups include cholesterols, lipids, phospholipids, biotin, phenazine, folate, phenanthridine, anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes. Groups that enhance the pharmacodynamic properties, in the context of this invention, include groups that improve uptake, enhance resistance to degradation, and/or strengthen sequence-specific hybridization with the target nucleic acid. Groups

that enhance the pharmacokinetic properties, in the context of this invention, include groups that improve uptake, distribution, metabolism or excretion of the compounds of the present invention. Representative conjugate groups are disclosed in International Patent Application PCT/US92/09196, filed October 23, 1992, and U.S. Patent No. 6,287,860, the entire disclosure of which are incorporated herein by reference. Conjugate moieties include but are not limited to lipid moieties such as a cholesterol moiety, cholic acid, a thioether, e.g., hexyl-S-tritylthiol, a thiocholesterol, an aliphatic chain, e.g., dodecandiol or undecyl residues, a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate, a polyamine or a polyethylene glycol chain, or adamantane acetic acid, a palmityl moiety, or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety. Oligonucleotides of the invention may also be conjugated to active drug substances, for example, aspirin, warfarin, phenylbutazone, ibuprofen, suprofen, fenbufen, ketoprofen, (*S*)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indomethicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic. Oligonucleotide-drug conjugates and their preparation are described in U.S. Patent Application No. 09/334,130 (filed June 15, 1999), which is incorporated herein by reference in its entirety.

Representative United States patents that teach the preparation of such oligonucleotide conjugates include, but are not limited to, U.S. Patent Nos.: 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538;

5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference.

Chimeric compounds

It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide.

The present invention also includes antisense compounds that are chimeric compounds. "Chimeric" antisense compounds or "chimeras," in the context of this invention, are antisense compounds, particularly oligonucleotides, which contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide in the case of an oligonucleotide compound. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, increased stability and/or increased binding affinity for the target nucleic

acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNAse H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNAse H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide-mediated inhibition of gene expression. The cleavage of RNA:RNA hybrids can, in like fashion, be accomplished through the actions of endoribonucleases, such as RNAseL which cleaves both cellular and viral RNA. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

In one embodiment, desirable chimeric oligonucleotides are 20 nucleotides in length, composed of a central region consisting of ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by five 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside linkages are phosphorothioate throughout the oligonucleotide and all cytidine residues are 5-methylcytidines.

In another embodiment, certain preferred chimeric oligonucleotides are those disclosed in the Examples herein. Particularly preferred chimeric oligonucleotides are those referred to as ISIS 304757, ISIS 304758, ISIS 304755, ISIS304800, and ISIS 304756.

Chimeric antisense compounds of the invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above. Such compounds have also been referred to in the art as hybrids or gapmers. Representative United

States patents that teach the preparation of such hybrid structures include, but are not limited to, U.S. Patent Nos.: 5,013,830; 5,149,797; 5,220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; and 5,700,922, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference in its entirety.

G. Formulations

The compounds of the invention may also be admixed, encapsulated, conjugated or otherwise associated with other molecules, molecule structures or mixtures of compounds, as for example, liposomes, receptor-targeted molecules, oral, rectal, topical or other formulations, for assisting in uptake, distribution and/or absorption. Representative United States patents that teach the preparation of such uptake, distribution and/or absorption-assisting formulations include, but are not limited to, U.S. Patent Nos.: 5,108,921; 5,354,844; 5,416,016; 5,459,127; 5,521,291; 5,543,158; 5,547,932; 5,583,020; 5,591,721; 4,426,330; 4,534,899; 5,013,556; 5,108,921; 5,213,804; 5,227,170; 5,264,221; 5,356,633; 5,395,619; 5,416,016; 5,417,978; 5,462,854; 5,469,854; 5,512,295; 5,527,528; 5,534,259; 5,543,152; 5,556,948; 5,580,575; and 5,595,756, each of which is herein incorporated by reference.

The antisense compounds of the invention encompass any pharmaceutically acceptable salts, esters, or salts of such esters, or any other compound which, upon administration to an animal, including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to prodrugs and pharmaceutically

acceptable salts of the compounds of the invention, pharmaceutically acceptable salts of such prodrugs, and other bioequivalents. The term "prodrug" indicates a therapeutic agent that is prepared in an inactive form that is converted to an active form (i.e., drug) within the body or cells thereof by the action of endogenous enzymes or other chemicals and/or conditions. In particular, prodrug versions of the oligonucleotides of the invention are prepared as SATE [(S-acetyl-2-thioethyl) phosphate] derivatives according to the methods disclosed in International Patent Application Publication No. WO 93/24510 to Gosselin *et al.*, published December 9, 1993, or in International Patent Publication No. WO 94/26764 and U.S. Patent No. 5,770,713 to Imbach *et al.*

The term "pharmaceutically acceptable salts" refers to physiologically and pharmaceutically acceptable salts of the compounds of the invention: i.e., salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto. For oligonucleotides, preferred examples of pharmaceutically acceptable salts and their uses are further described in U.S. Patent No. 6,287,860, which is incorporated herein in its entirety.

The present invention also includes pharmaceutical compositions and formulations that include the antisense compounds of the invention. The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical (including ophthalmic and to mucous membranes including vaginal and rectal delivery), pulmonary, e.g., by inhalation or insufflation of powders or aerosols, including

by nebulizer; intratracheal, intranasal, epidermal and transdermal), oral or parenteral. Parenteral administration includes intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; or intracranial, e.g., intrathecal or intraventricular, administration. Oligonucleotides with at least one 2'-O-methoxyethyl modification are believed to be particularly useful for oral administration. Pharmaceutical compositions and formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Coated condoms, gloves and the like may also be useful.

The pharmaceutical formulations of the present invention, which may conveniently be presented in unit dosage form, may be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

The compositions of the present invention may be formulated into any of many possible dosage forms such as, but not limited to, tablets, capsules, gel capsules, liquid syrups, soft gels, suppositories, and enemas. The compositions of the present invention may also be formulated as suspensions in aqueous, non-aqueous or mixed media.

Aqueous suspensions may further contain substances that increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension may also contain stabilizers.

Pharmaceutical compositions of the present invention include, but are not limited to, solutions, emulsions, foams and liposome-containing formulations. The pharmaceutical compositions and formulations of the present invention may comprise one or more penetration enhancers, carriers, excipients or other active or inactive ingredients.

Emulsions are typically heterogenous systems of one liquid dispersed in another in the form of droplets usually exceeding 0.1 μm in diameter. Emulsions may contain additional components in addition to the dispersed phases, and the active drug that may be present as a solution in either the aqueous phase, oily phase or itself as a separate phase. Microemulsions are included as an embodiment of the present invention. Emulsions and their uses are well known in the art and are further described in U.S. Patent No. 6,287,860, which is incorporated herein in its entirety.

Formulations of the present invention include liposomal formulations. As used in the present invention, the term "liposome" means a vesicle composed of amphiphilic lipids arranged in a spherical bilayer or bilayers. Liposomes are unilamellar or multilamellar vesicles which have a membrane formed from a lipophilic material and an aqueous interior that contains the composition to be delivered. Cationic liposomes are positively charged liposomes, which are believed to interact with negatively charged DNA molecules to form a stable complex. Liposomes that are pH-sensitive or negatively-charged are believed to entrap DNA rather than

complex with it. Both cationic and noncationic liposomes have been used to deliver DNA to cells.

Liposomes also include "sterically stabilized" liposomes, a term that, as used herein, refers to liposomes comprising one or more specialized lipids that, when incorporated into liposomes, result in enhanced circulation lifetimes relative to liposomes lacking such specialized lipids. Examples of sterically stabilized liposomes are those in which part of the vesicle-forming lipid portion of the liposome comprises one or more glycolipids or is derivatized with one or more hydrophilic polymers, such as a polyethylene glycol (PEG) moiety. Liposomes and their uses are further described in U.S. Patent No. 6,287,860, which is incorporated herein in its entirety.

The pharmaceutical formulations and compositions of the present invention may also include surfactants. The use of surfactants in drug products, formulations and in emulsions is well known in the art. Surfactants and their uses are further described in U.S. Patent No. 6,287,860, which is incorporated herein in its entirety.

In one embodiment, the present invention employs various penetration enhancers to affect the efficient delivery of nucleic acids, particularly oligonucleotides. In addition to aiding the diffusion of non-lipophilic drugs across cell membranes, penetration enhancers also enhance the permeability of lipophilic drugs. Penetration enhancers may be classified as belonging to one of five broad categories, *i.e.*, surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants. Penetration enhancers and their uses are further described in U.S. Patent No. 6,287,860, which is incorporated herein in its entirety.

One of skill in the art will recognize that formulations are routinely designed according to their intended use, i.e. route of administration.

Preferred formulations for topical administration include those in which the oligonucleotides of the invention are in admixture with a topical delivery agent such as lipids, liposomes, fatty acids, fatty acid esters, steroids, chelating agents and surfactants. Preferred lipids and liposomes include neutral (e.g. dioleoylphosphatidyl DOPE ethanolamine, dimyristoylphosphatidyl choline DMPC, distearolyphosphatidyl choline) negative (e.g. dimyristoylphosphatidyl glycerol DMPG) and cationic (e.g. dioleoyltetramethylaminopropyl DOTAP and dioleoylphosphatidyl ethanolamine DOTMA).

For topical or other administration, oligonucleotides of the invention may be encapsulated within liposomes or may form complexes thereto, in particular to cationic liposomes. Alternatively, oligonucleotides may be complexed to lipids, in particular to cationic lipids. Preferred fatty acids and esters, pharmaceutically acceptable salts thereof, and their uses are further described in U.S. Patent No. 6,287,860, which is incorporated herein in its entirety. Topical formulations are described in detail in U.S. Patent Application No. 09/315,298, filed on May 20, 1999, which is incorporated herein by reference in its entirety.

Compositions and formulations for oral administration include powders or granules, microparticulates, nanoparticulates, suspensions or solutions in water or non-aqueous media, capsules, gel capsules, sachets, tablets or minitablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable. Preferred oral formulations are those in which

oligonucleotides of the invention are administered in conjunction with one or more penetration enhancers surfactants and chelators. Preferred surfactants include fatty acids and/or esters or salts thereof, bile acids and/or salts thereof. Preferred bile acids/salts and fatty acids and their uses are further described in U.S. Patent No. 6,287,860, which is incorporated herein in its entirety. Also preferred are combinations of penetration enhancers, for example, fatty acids/salts in combination with bile acids/salts. A particularly preferred combination is the sodium salt of lauric acid, capric acid and UDCA. Further penetration enhancers include polyoxyethylene-9-lauryl ether, polyoxyethylene-20-cetyl ether. Oligonucleotides of the invention may be delivered orally, in granular form including sprayed dried particles, or complexed to form micro or nanoparticles. Oligonucleotide complexing agents and their uses are further described in U.S. Patent No. 6,287,860, which is incorporated herein in its entirety. Oral formulations for oligonucleotides and their preparation are described in detail in U.S. Published Patent Application No. 2003/0040497 (February 27, 2003) and its parent applications; U.S. Published Patent Application No. 2003/0027780 (February 6, 2003) and its parent applications; and U.S. Patent Application No. 10/071,822, filed February 8, 2002, each of which is incorporated herein by reference in their entirety.

Compositions and formulations for parenteral, intrathecal or intraventricular administration may include sterile aqueous solutions that may also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients.

Certain embodiments of the invention provide pharmaceutical compositions containing one or more oligomeric compounds and one or more other chemotherapeutic agents, which function by a non-antisense mechanism. Examples of such chemotherapeutic agents include but are not limited to cancer chemotherapeutic drugs such as daunorubicin, daunomycin, dactinomycin, doxorubicin, epirubicin, idarubicin, esorubicin, bleomycin, mafosfamide, ifosfamide, cytosine arabinoside, bis-chloroethylnitrosurea, busulfan, mitomycin C, actinomycin D, mithramycin, prednisone, hydroxyprogesterone, testosterone, tamoxifen, dacarbazine, procarbazine, hexamethylmelamine, pentamethylmelamine, mitoxantrone, amsacrine, chlorambucil, methylcyclohexylnitrosurea, nitrogen mustards, melphalan, cyclophosphamide, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-azacytidine, hydroxyurea, deoxycoformycin, 4-hydroxyperoxycyclophosphoramide, 5-fluorouracil (5-FU), 5-fluorodeoxyuridine (5-FUdR), methotrexate (MTX), colchicine, taxol, vincristine, vinblastine, etoposide (VP-16), trimetrexate, irinotecan, topotecan, gemcitabine, teniposide, cisplatin and diethylstilbestrol (DES). When used with the compounds of the invention, such chemotherapeutic agents may be used individually (*e.g.*, 5-FU and oligonucleotide), sequentially (*e.g.*, 5-FU and oligonucleotide for a period of time followed by MTX and oligonucleotide), or in combination with one or more other such chemotherapeutic agents (*e.g.*, 5-FU, MTX and oligonucleotide, or 5-FU, radiotherapy and oligonucleotide). Anti-inflammatory drugs, including but not limited to nonsteroidal anti-inflammatory drugs and corticosteroids, and antiviral drugs, including but not limited to ribivirin, vidarabine, acyclovir and ganciclovir, may also be combined

in compositions of the invention. Combinations of antisense compounds and other non-antisense drugs are also within the scope of this invention. Two or more combined compounds may be used together or sequentially.

In another related embodiment, compositions of the invention may contain one or more antisense compounds, particularly oligonucleotides, targeted to a first nucleic acid and one or more additional antisense compounds targeted to a second nucleic acid target. Alternatively, compositions of the invention may contain two or more antisense compounds targeted to different regions of the same nucleic acid target. Numerous examples of antisense compounds are known in the art. Two or more combined compounds may be used together or sequentially.

H. Dosing

The formulation of therapeutic compositions and their subsequent administration (dosing) is believed to be within the skill of those in the art. Dosing is dependent on severity and responsiveness of the disease state to be treated, with the course of treatment lasting from several days to several months, or until a cure is effected or a diminution of the disease state is achieved. Optimal dosing schedules can be calculated from measurements of drug accumulation in the body of the patient. Persons of ordinary skill can easily determine optimum dosages, dosing methodologies and repetition rates. Optimum dosages may vary depending on the relative potency of individual oligonucleotides, and can generally be estimated based on EC_{50}s found to be effective in *in vitro* and *in vivo* animal models. In general, dosage is from 0.01 μg to 100 g per kg of body weight, and may be given once or more daily, weekly,

monthly or yearly, or even once every 2 to 20 years. Persons of ordinary skill in the art can easily estimate repetition rates for dosing based on measured residence times and concentrations of the drug in bodily fluids or tissues. Following successful treatment, it may be desirable to have the patient undergo maintenance therapy to prevent the recurrence of the disease state, wherein the oligonucleotide is administered in maintenance doses, ranging from 0.01 μg to 100 g per kg of body weight, once or more daily, to once every 20 years.

While the present invention has been described with specificity in accordance with certain of its preferred embodiments, the following examples serve only to illustrate the invention and are not intended to limit the same.

EXAMPLES

Example 1: Synthesis of Nucleoside Phosphoramidites

The following compounds, including amidites and their intermediates were prepared as described in U.S. Patent No. 6,426,220 and International Patent Publication No. WO 02/36743; 5'-O-Dimethoxytrityl-thymidine intermediate for 5-methyl dC amidite, 5'-O-Dimethoxytrityl-2'-deoxy-5-methylcytidine intermediate for 5-methyl-dC amidite, 5'-O-Dimethoxytrityl-2'-deoxy-N4-benzoyl-5-methylcytidine penultimate intermediate for 5-methyl dC amidite, [5'-*O*-(4,4'-Dimethoxytriphenylmethyl)-2'-deoxy-N^4-benzoyl-5-methylcytidin-3'-*O*-yl]-2-cyanoethyl-*N*,*N*-diisopropylphosphoramidite (5-methyl dC amidite), 2'-Fluorodeoxyadenosine, 2'-Fluorodeoxyguanosine, 2'-Fluorouridine, 2'-Fluorodeoxycytidine, 2'-O-(2-Methoxyethyl) modified amidites, 2'-O-(2-methoxyethyl)-5-methyluridine

intermediate, 5'-O-DMT-2'-O-(2-methoxyethyl)-5-methyluridine penultimate intermediate, [5'-*O*-(4,4'-Dimethoxytriphenylmethyl)-2'-*O*-(2-methoxyethyl)-5-methyluridin-3'-*O*-yl]-2-cyanoethyl-*N,N*-diisopropylphosphoramidite (MOE T amidite), 5'-O-Dimethoxytrityl-2'-O-(2-methoxyethyl)-5-methylcytidine intermediate, 5'-O-dimethoxytrityl-2'-*O*-(2-methoxyethyl)-N^4-benzoyl-5-methyl-cytidine penultimate intermediate, [5'-*O*-(4,4'-Dimethoxytriphenylmethyl)-2'-*O*-(2-methoxyethyl)-N^4-benzoyl-5-methylcytidin-3'-*O*-yl]-2-cyanoethyl-*N,N*-diisopropylphosphoramidite (MOE 5-Me-C amidite), [5'-*O*-(4,4'-Dimethoxytriphenylmethyl)-2'-*O*-(2-methoxyethyl)-N^6-benzoyladenosin-3'-*O*-yl]-2-cyanoethyl-*N,N*-diisopropylphosphoramidite (MOE A amidite), [5'-*O*-(4,4'-Dimethoxytriphenylmethyl)-2'-*O*-(2-methoxyethyl)-N^4-isobutyrylguanosin-3'-*O*-yl]-2-cyanoethyl-*N,N*-diisopropylphosphoramidite (MOE G amidite), 2′-O-(Aminooxyethyl) nucleoside amidites and 2′-O-(dimethylamino-oxyethyl) nucleoside amidites, 2'-(Dimethylaminooxyethoxy) nucleoside amidites, 5'-O-tert-Butyldiphenylsilyl-O^2-2'-anhydro-5-methyluridine , 5'-O-tert-Butyldiphenylsilyl-2'-O-(2-hydroxyethyl)-5-methyluridine, 2'-O-([2-phthalimidoxy)ethyl]-5'-*t*-butyldiphenylsilyl-5-methyluridine , 5'-O-*tert*-butyldiphenylsilyl-2'-O-[(2-formadoximinooxy)ethyl]-5-methyluridine, 5'-O-*tert*-Butyldiphenylsilyl-2'-O-[N,N dimethylaminooxyethyl]-5-methyluridine, 2'-O-(dimethylaminooxyethyl)-5-methyluridine, 5'-O-DMT-2'-O-(dimethylaminooxyethyl)-5-methyluridine, 5'-O-DMT-2'-O-(2-N,N-dimethylaminooxyethyl)-5-methyluridine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite], 2'-(Aminooxyethoxy) nucleoside amidites, N2-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-

dimethoxytrityl)guanosine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite], 2'-dimethylaminoethoxyethoxy (2'-DMAEOE) nucleoside amidites, 2'-O-[2(2-N,N-dimethylaminoethoxy)ethyl]-5-methyl uridine, 5'-O-dimethoxytrityl-2'-O-[2(2-N,N-dimethylaminoethoxy)-ethyl)]-5-methyl uridine and 5'-O-Dimethoxytrityl-2'-O-[2(2-N,N-dimethylaminoethoxy)-ethyl)]-5-methyl uridine-3'-O-(cyanoethyl-N,N-diisopropyl)phosphoramidite.

Example 2: Oligonucleotide and oligonucleoside synthesis

The antisense compounds used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, CA). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives.

Oligonucleotides: Unsubstituted and substituted phosphodiester (P=O) oligonucleotides are synthesized on an automated DNA synthesizer (Applied Biosystems model 394) using standard phosphoramidite chemistry with oxidation by iodine.

Phosphorothioates (P=S) are synthesized similar to phosphodiester oligonucleotides with the following exceptions: thiation was effected by utilizing a 10% w/v solution of 3,H-1,2-benzodithiole-3-one 1,1-dioxide in acetonitrile for the oxidation of the phosphite linkages. The thiation reaction step time was increased to 180 sec and preceded by the normal capping step. After cleavage from the CPG column and deblocking in concentrated ammonium

hydroxide at 55°C (12-16 hr), the oligonucleotides were recovered by precipitating with >3 volumes of ethanol from a 1 M NH_4OAc solution. Phosphinate oligonucleotides are prepared as described in U.S. Patent No. 5,508,270, herein incorporated by reference.

Alkyl phosphonate oligonucleotides are prepared as described in U.S. Patent No. 4,469,863, herein incorporated by reference.

3'-Deoxy-3'-methylene phosphonate oligonucleotides are prepared as described in U.S. Patent Nos. 5,610,289 or 5,625,050, herein incorporated by reference.

Phosphoramidite oligonucleotides are prepared as described in U.S. Patent Nos. 5,256,775 or 5,366,878, herein incorporated by reference.

Alkylphosphonothioate oligonucleotides are prepared as described in International Patent Application Nos. PCT/US94/00902 and PCT/US93/06976 (published as WO 94/17093 and WO 94/02499, respectively), herein incorporated by reference.

3'-Deoxy-3'-amino phosphoramidate oligonucleotides are prepared as described in U.S. Patent No. 5,476,925, herein incorporated by reference.

Phosphotriester oligonucleotides are prepared as described in U.S. Patent No. 5,023,243, herein incorporated by reference.

Borano phosphate oligonucleotides are prepared as described in U.S. Patent Nos. 5,130,302 and 5,177,198, both herein incorporated by reference.

Oligonucleosides: Methylenemethylimino linked oligonucleosides, also identified as MMI linked oligonucleosides, methylenedimethylhydrazo linked oligonucleosides, also identified as MDH linked

oligonucleosides, and methylenecarbonylamino linked oligonucleosides, also identified as amide-3 linked oligonucleosides, and methyleneaminocarbonyl linked oligonucleosides, also identified as amide-4 linked oligonucleosides, as well as mixed backbone compounds having, for instance, alternating MMI and P=O or P=S linkages are prepared as described in U.S. Patent Nos. 5,378,825, 5,386,023, 5,489,677, 5,602,240 and 5,610,289, all of which are herein incorporated by reference.

Formacetal and thioformacetal linked oligonucleosides are prepared as described in U.S. Patent Nos. 5,264,562 and 5,264,564, herein incorporated by reference.

Ethylene oxide linked oligonucleosides are prepared as described in U.S. Patent No. 5,223,618, herein incorporated by reference.

Example 3: RNA Synthesis

In general, RNA synthesis chemistry is based on the selective incorporation of various protecting groups at strategic intermediary reactions. Although one of ordinary skill in the art will understand the use of protecting groups in organic synthesis, a useful class of protecting groups includes silyl ethers. In particular bulky silyl ethers are used to protect the 5´-hydroxyl in combination with an acid-labile orthoester protecting group on the 2´-hydroxyl. This set of protecting groups is then used with standard solid-phase synthesis technology. It is important to lastly remove the acid labile orthoester protecting group after all other synthetic steps. Moreover, the early use of the silyl protecting groups during synthesis ensures facile removal when desired, without undesired deprotection of 2´ hydroxyl.

Following this procedure for the sequential protection of the 5´-hydroxyl in combination with protection of the 2´-hydroxyl by protecting groups that are differentially removed and are differentially chemically labile, RNA oligonucleotides were synthesized.

RNA oligonucleotides are synthesized in a stepwise fashion. Each nucleotide is added sequentially (3´- to 5´-direction) to a solid support-bound oligonucleotide. The first nucleoside at the 3´-end of the chain is covalently attached to a solid support. The nucleotide precursor, a ribonucleoside phosphoramidite, and activator are added, coupling the second base onto the 5´-end of the first nucleoside. The support is washed and any unreacted 5´-hydroxyl groups are capped with acetic anhydride to yield 5´-acetyl moieties. The linkage is then oxidized to the more stable and ultimately desired P(V) linkage. At the end of the nucleotide addition cycle, the 5´-silyl group is cleaved with fluoride. The cycle is repeated for each subsequent nucleotide.

Following synthesis, the methyl protecting groups on the phosphates are cleaved in 30 minutes utilizing 1 M disodium-2-carbamoyl-2-cyanoethylene-1,1-dithiolate trihydrate (S_2Na_2) in DMF. The deprotection solution is washed from the solid support-bound oligonucleotide using water. The support is then treated with 40% methylamine in water for 10 minutes at 55 °C. This releases the RNA oligonucleotides into solution, deprotects the exocyclic amines, and modifies the 2´- groups. The oligonucleotides can be analyzed by anion exchange HPLC at this stage.

The 2´-orthoester groups are the last protecting groups to be removed. The ethylene glycol monoacetate orthoester protecting group developed by Dharmacon Research, Inc.

(Lafayette, CO), is one example of a useful orthoester protecting group, which has the following important properties. It is stable to the conditions of nucleoside phosphoramidite synthesis and oligonucleotide synthesis. However, after oligonucleotide synthesis the oligonucleotide is treated with methylamine, which not only cleaves the oligonucleotide from the solid support but also removes the acetyl groups from the orthoesters. The resulting 2-ethyl-hydroxyl substituents on the orthoester are less-electron withdrawing than the acetylated precursor. As a result, the modified orthoester becomes more labile to acid-catalyzed hydrolysis. Specifically, the rate of cleavage is approximately 10 times faster after the acetyl groups are removed. Therefore, this orthoester possesses sufficient stability in order to be compatible with oligonucleotide synthesis and yet, when subsequently modified, permits deprotection to be carried out under relatively mild aqueous conditions compatible with the final RNA oligonucleotide product.

Additionally, methods of RNA synthesis are well known in the art (Scaringe, S. A. Ph.D. Thesis, University of Colorado, 1996; Scaringe, S. A., *et al.*, *J. Am. Chem. Soc.*, **1998**, *120*, 11820-11821; Matteucci, M. D. and Caruthers, M. H. *J. Am. Chem. Soc.*, **1981**, *103*, 3185-3191; Beaucage, S. L. and Caruthers, M. H. *Tetrahedron Lett.*, **1981**, *22*, 1859-1862; Dahl, B. J., *et al.*, *Acta Chem. Scand*,. **1990**, *44*, 639-641; Reddy, M. P., *et al.*, *Tetrahedrom Lett.*, **1994**, *25*, 4311-4314; Wincott, F. *et al.*, *Nucleic Acids Res.*, **1995**, *23*, 2677-2684; Griffin, B. E., *et al.*, *Tetrahedron*, **1967**, *23*, 2301-2313; Griffin, B. E., *et al.*, *Tetrahedron*, **1967**, *23*, 2315-2331).

RNA antisense compounds (RNA oligonucleotides) of the present invention can be synthesized by the methods herein or purchased from Dharmacon Research, Inc (Lafayette, CO). Once synthesized, complementary RNA antisense compounds can then be annealed by methods known in the art to form double stranded (duplexed) antisense compounds. For example, duplexes can be formed by combining 30 μl of each of the complementary strands of RNA oligonucleotides (50 uM RNA oligonucleotide solution) and 15 μl of 5X annealing buffer (100 mM potassium acetate, 30 mM HEPES-KOH pH 7.4, 2 mM magnesium acetate) followed by heating for 1 minute at 90°C, then 1 hour at 37°C. The resulting duplexed antisense compounds can be used in kits, assays, screens, or other methods to investigate the role of a target nucleic acid.

Example 4: Synthesis of Chimeric Oligonucleotides

Chimeric oligonucleotides, oligonucleosides or mixed oligonucleotides/oligonucleosides of the invention can be of several different types. These include a first type wherein the "gap" segment of linked nucleosides is positioned between 5' and 3' "wing" segments of linked nucleosides and a second "open end" type wherein the "gap" segment is located at either the 3' or the 5' terminus of the oligomeric compound. Oligonucleotides of the first type are also known in the art as "gapmers" or gapped oligonucleotides. Oligonucleotides of the second type are also known in the art as "hemimers" or "wingmers".

[2'-O-Me]--[2'-deoxy]--[2'-O-Me] Chimeric Phosphorothioate Oligonucleotides

Chimeric oligonucleotides having 2'-O-alkyl phosphorothioate and 2'-deoxy phosphorothioate oligo-

nucleotide segments are synthesized using an Applied Biosystems automated DNA synthesizer Model 394, as above. Oligonucleotides are synthesized using the automated synthesizer and 2'-deoxy-5'-dimethoxytrityl-3'-O-phosphoramidite for the DNA portion and 5'-dimethoxytrityl-2'-O-methyl-3'-O-phosphoramidite for 5' and 3' wings. The standard synthesis cycle is modified by incorporating coupling steps with increased reaction times for the 5'-dimethoxytrityl-2'-O-methyl-3'-O-phosphoramidite. The fully protected oligonucleotide is cleaved from the support and deprotected in concentrated ammonia (NH_4OH) for 12-16 hr at 55°C. The deprotected oligo is then recovered by an appropriate method (precipitation, column chromatography, volume reduced *in vacuo* and analyzed spectrophotometrically for yield and for purity by capillary electrophoresis and by mass spectrometry.

[2'-O-(2-Methoxyethyl)]--[2'-deoxy]--[2'-O-(Methoxyethyl)] Chimeric Phosphorothioate Oligonucleotides

[2'-O-(2-methoxyethyl)]--[2'-deoxy]--[-2'-O-(methoxyethyl)] chimeric phosphorothioate oligonucleotides were prepared as per the procedure above for the 2'-O-methyl chimeric oligonucleotide, with the substitution of 2'-O-(methoxyethyl) amidites for the 2'-O-methyl amidites.

[2'-O-(2-Methoxyethyl)Phosphodiester]--[2'-deoxy Phosphorothioate]--[2'-O-(2-Methoxyethyl) Phosphodiester] Chimeric Oligonucleotides

[2'-O-(2-methoxyethyl phosphodiester]--[2'-deoxy phosphorothioate]--[2'-O-(methoxyethyl) phosphodiester] chimeric oligonucleotides are prepared as per the above

procedure for the 2′-O-methyl chimeric oligonucleotide with the substitution of 2′-O-(methoxyethyl) amidites for the 2′-O-methyl amidites, oxidation with iodine to generate the phosphodiester internucleotide linkages within the wing portions of the chimeric structures and sulfurization utilizing 3,H-1,2 benzodithiole-3-one 1,1 dioxide (Beaucage Reagent) to generate the phosphorothioate internucleotide linkages for the center gap.

Other chimeric oligonucleotides, chimeric oligonucleosides and mixed chimeric oligonucleotides/oligonucleosides are synthesized according to United States Patent No. 5,623,065, herein incorporated by reference.

Example 5: Design and screening of duplexed antisense compounds targeting apolipoprotein C-III

In accordance with the present invention, a series of nucleic acid duplexes comprising the antisense compounds of the present invention and their complements are designed to target apolipoprotein C-III. The nucleobase sequence of the antisense strand of the duplex comprises at least a portion of an oligonucleotide in Table 1. The ends of the strands may be modified by the addition of one or more natural or modified nucleobases to form an overhang. The sense strand of the dsRNA is then designed and synthesized as the complement of the antisense strand and may also contain modifications or additions to either terminus. For example, in one embodiment, both strands of the dsRNA duplex would be complementary over the central nucleobases, each having overhangs at one or both termini.

For example, a duplex comprising an antisense strand having the sequence CGAGAGGCGGACGGGACCG (SEQ ID NO: 465) and

having a two-nucleobase overhang of deoxythymidine(dT) would have the following structure (Antisense SEQ ID NO: 466, Complement SEQ ID NO: 467):

```
  cgagaggcggacgggaccgTT    Antisense Strand
  |||||||||||||||||||
TTgctctccgcctgccctggc      Complement
```

In another embodiment, a duplex comprising an antisense strand having the same sequence CGAGAGGCGGACGGGACCG (SEQ ID NO: 465) may be prepared with blunt ends (no single stranded overhang) as shown (Antisense SEQ ID NO: 465, Complement SEQ ID NO: 468):

```
cgagaggcggacgggaccg    Antisense Strand
|||||||||||||||||||
gctctccgcctgccctggc    Complement
```

RNA strands of the duplex can be synthesized by methods disclosed herein or purchased from Dharmacon Research Inc., (Lafayette, CO). Once synthesized, the complementary strands are annealed. The single strands are aliquoted and diluted to a concentration of 50 μM. Once diluted, 30 μL of each strand is combined with 15μL of a 5X solution of annealing buffer. The final concentration of said buffer is 100 mM potassium acetate, 30 mM HEPES-KOH pH 7.4, and 2mM magnesium acetate. The final volume is 75 μL. This solution is incubated for 1 minute at 90°C and then centrifuged for 15 seconds. The tube is allowed to sit for 1 hour at 37°C at which time the dsRNA duplexes are used in experimentation. The final concentration of the dsRNA duplex is 20 μM. This solution can be stored frozen (-20°C) and freeze-thawed up to 5 times.

Once prepared, the duplexed antisense compounds are evaluated for their ability to modulate apolipoprotein C-III expression.

When cells reached 80% confluency, they are treated with duplexed antisense compounds of the invention. For cells grown in 96-well plates, wells are washed once with 200 µL OPTI-MEM-1™ reduced-serum medium (Gibco BRL) and then treated with 130 µL of OPTI-MEM-1™ medium containing 12 µg/mL LIPOFECTIN™ reagent (Gibco BRL) and the desired duplex antisense compound at a final concentration of 200 nM. After 5 hours of treatment, the medium is replaced with fesh medium. Cells are harvested 16 hours after treatment, at which time RNA is isolated and target reduction measured by RT-PCR.

Example 6: Oligonucleotide Isolation

After cleavage from the controlled pore glass solid support and deblocking in concentrated ammonium hydroxide at 55°C for 12-16 hours, the oligonucleotides or oligonucleosides are recovered by precipitation out of 1 M NH_4OAc with >3 volumes of ethanol. Synthesized oligonucleotides were analyzed by electrospray mass spectroscopy (molecular weight determination) and by capillary gel electrophoresis and judged to be at least 70% full-length material. The relative amounts of phosphorothioate and phosphodiester linkages obtained in the synthesis were determined by the ratio of correct molecular weight relative to the −16 amu product (+/-32 +/-48). For some studies oligonucleotides were purified by HPLC, as described by Chiang *et al.*, *J. Biol. Chem.* **1991**, *266*, 18162-18171. Results obtained with HPLC-purified material were similar to those obtained with non-HPLC purified material.

Example 7: Oligonucleotide Synthesis - 96 Well Plate Format

Oligonucleotides were synthesized via solid phase P(III) phosphoramidite chemistry on an automated synthesizer capable of assembling 96 sequences simultaneously in a 96-well format. Phosphodiester internucleotide linkages were afforded by oxidation with aqueous iodine. Phosphorothioate internucleotide linkages were generated by sulfurization utilizing 3,H-1,2 benzodithiole-3-one 1,1 dioxide (Beaucage Reagent) in anhydrous acetonitrile. Standard base-protected beta-cyanoethyl-diiso-propyl phosphoramidites were purchased from commercial vendors (e.g. PE-Applied Biosystems, Foster City, CA, or Pharmacia, Piscataway, NJ). Non-standard nucleosides are synthesized as per standard or patented methods. They are utilized as base protected beta-cyanoethyldiisopropyl phosphoramidites.

Oligonucleotides were cleaved from support and deprotected with concentrated NH_4OH at elevated temperature (55-60°C) for 12-16 hours and the released product then dried *in vacuo*. The dried product was then re-suspended in sterile water to afford a master plate from which all analytical and test plate samples are then diluted utilizing robotic pipettors.

Example 8: Oligonucleotide Analysis - 96-Well Plate Format

The concentration of oligonucleotide in each well was assessed by dilution of samples and UV absorption spectroscopy. The full-length integrity of the individual products was evaluated by capillary electrophoresis (CE) in either the 96-well format (Beckman P/ACE™ MDQ apparatus) or, for individually prepared samples, on a commercial CE apparatus (e.g., Beckman P/ACE™ 5000, ABI 270 apparatus). Base and backbone composition was confirmed by mass analysis

of the compounds utilizing electrospray-mass spectroscopy. All assay test plates were diluted from the master plate using single and multi-channel robotic pipettors. Plates were judged to be acceptable if at least 85% of the compounds on the plate were at least 85% full length.

Example 9: Cell culture and oligonucleotide treatment

The effect of antisense compounds on target nucleic acid expression can be tested in any of a variety of cell types provided that the target nucleic acid is present at measurable levels. This can be routinely determined using, for example, PCR or Northern blot analysis. The following cell types are provided for illustrative purposes, but other cell types can be routinely used, provided that the target is expressed in the cell type chosen. This can be readily determined by methods routine in the art, for example Northern blot analysis, ribonuclease protection assays, or RT-PCR.

T-24 cells:

The human transitional cell bladder carcinoma cell line T-24 was obtained from the American Type Culture Collection (ATCC) (Manassas, VA). T-24 cells were routinely cultured in complete McCoy's 5A basal media (Invitrogen Corporation, Carlsbad, CA) supplemented with 10% fetal calf serum (Invitrogen Corporation, Carlsbad, CA), penicillin 100 units per mL, and streptomycin 100 micrograms per mL (Invitrogen Corporation, Carlsbad, CA). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence. Cells were seeded into 96-well plates (Falcon-Primaria #353872) at a density of 7000 cells/well for use in RT-PCR analysis.

For Northern blotting or other analysis, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide.

A549 cells:

The human lung carcinoma cell line A549 was obtained from the American Type Culture Collection (ATCC) (Manassas, VA). A549 cells were routinely cultured in DMEM basal media (Invitrogen Corporation, Carlsbad, CA) supplemented with 10% fetal calf serum (Invitrogen Corporation, Carlsbad, CA), penicillin 100 units per mL, and streptomycin 100 micrograms per mL (Invitrogen Corporation, Carlsbad, CA). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence.

NHDF cells:

Human neonatal dermal fibroblast (NHDF) were obtained from the Clonetics Corporation (Walkersville, MD). NHDFs were routinely maintained in Fibroblast Growth Medium (Clonetics Corporation, Walkersville, MD) supplemented as recommended by the supplier. Cells were maintained for up to 10 passages as recommended by the supplier.

HEK cells:

Human embryonic keratinocytes (HEK) were obtained from the Clonetics Corporation (Walkersville, MD). HEKs were routinely maintained in Keratinocyte Growth Medium (Clonetics Corporation, Walkersville, MD) formulated as recommended by the supplier. Cells were routinely maintained for up to 10 passages as recommended by the supplier.

HepG2 cells:

The human hepatoblastoma cell line HepG2 was obtained from the American Type Culture Collection (Manassas, VA). HepG2 cells were routinely cultured in Eagle's MEM supplemented with 10% fetal calf serum, non-essential amino acids, and 1 mM sodium pyruvate (Gibco/Life Technologies, Gaithersburg, MD). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence. Cells were seeded into 96-well plates (Falcon-Primaria #3872) at a density of 7000 cells/well for use in RT-PCR analysis.

For Northern blotting or other analyses, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide.

Hep3B cells:

The human hepatocellular carcinoma cell line Hep3B was obtained from the American Type Culture Collection (Manassas, VA). Hep3B cells were routinely cultured in Dulbeccos's MEM high glucose supplemented with 10% fetal calf serum, L-glutamine and pyridoxine hydrochloride (Gibco/Life Technologies, Gaithersburg, MD). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence. Cells were seeded into 24-well plates (Falcon-Primaria #3846) at a density of 50,000 cells/well for use in RT-PCR analysis.

For Northern blotting or other analyses, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide.

Primary mouse hepatocytes:

Primary mouse hepatocytes were prepared from CD-1 mice purchased from Charles River Labs (Wilmington, MA) and were routinely cultured in DMEM, high glucose (Invitrogen Life Technologies, Carlsbad, CA) supplemented with 10% fetal bovine serum (Invitrogen Life Technologies, Carlsbad, CA), 100 units per ml penicillin, and 100 micrograms per ml streptomycin (Invitrogen Life Technologies, Carlsbad, CA). Cells were cultured to 80% confluence for use in antisense oligonucleotide transfection experiments.

For Northern blotting or other analyses, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide.

Primary rat hepatocytes:

Primary rat hepatocytes were prepared from Sprague-Dawley rats purchased from Charles River Labs (Wilmington, MA) and were routinely cultured in DMEM, high glucose (Invitrogen Life Technologies, Carlsbad, CA) supplemented with 10% fetal bovine serum (Invitrogen Life Technologies, Carlsbad, CA), 100 units per ml penicillin, and 100 micrograms per ml streptomycin (Invitrogen Life Technologies, Carlsbad, CA). Cells were cultured to 80% confluence for use in antisense oligonucleotide transfection experiments.

Treatment with antisense compounds:

When cells reached 65-75% confluency, they were treated with oligonucleotide. For cells grown in 96-well plates, wells were washed once with 100 µL OPTI-MEM™-1 reduced-

serum medium (Invitrogen Life Technologies, Carlsbad, CA) and then treated with 130 µL of OPTI-MEM™-1 medium containing 3.75 µg/mL LIPOFECTIN™ reagent (Invitrogen Life Technologies, Carlsbad, CA) and the desired concentration of oligonucleotide. Cells are treated and data are obtained in triplicate. After 4-7 hours of treatment at 37°C, the medium was replaced with fresh medium. Cells were harvested 16-24 hours after oligonucleotide treatment.

The concentration of oligonucleotide used varies from cell line to cell line. To determine the optimal oligonucleotide concentration for a particular cell line, the cells are treated with a positive control oligonucleotide at a range of concentrations. For human cells the positive control oligonucleotide is selected from either ISIS 13920 (**TCC**GTCATCGCT**CCTCAGGG**, SEQ ID NO: 1) which is targeted to human H-ras, or ISIS 18078, (**GTGCG**CGCGAGCCCG**AAATC**, SEQ ID NO: 2) which is targeted to human Jun-N-terminal kinase-2 (JNK2). Both controls are 2'-O-methoxyethyl gapmers (2'-O-methoxyethyls shown in bold) with a phosphorothioate backbone. For mouse or rat cells the positive control oligonucleotide is ISIS 15770, **ATGCA**TTCTGCCCCC**AAGGA**, SEQ ID NO: 3, a 2'-O-methoxyethyl gapmer (2'-O-methoxyethyls shown in bold) with a phosphorothioate backbone which is targeted to both mouse and rat c-raf. The concentration of positive control oligonucleotide that results in 80% inhibition of c-H-ras (for ISIS 13920), JNK2 (for ISIS 18078) or c-raf (for ISIS 15770) mRNA is then utilized as the screening concentration for new oligonucleotides in subsequent experiments for that cell line. If 80% inhibition is not achieved, the lowest concentration of positive control oligonucleotide that results in 60% inhibition of c-H-ras, JNK2 or c-raf mRNA is

then utilized as the oligonucleotide screening concentration in subsequent experiments for that cell line. If 60% inhibition is not achieved, that particular cell line is deemed as unsuitable for oligonucleotide transfection experiments. The concentrations of antisense oligonucleotides used herein are from 50 nM to 300 nM.

Example 10: Analysis of oligonucleotide inhibition of apolipoprotein C-III expression

Antisense modulation of apolipoprotein C-III expression can be assayed in a variety of ways known in the art. For example, apolipoprotein C-III mRNA levels can be quantitated by, e.g., Northern blot analysis, competitive polymerase chain reaction (PCR), or real-time PCR (RT-PCR). Real-time quantitative PCR is presently preferred. RNA analysis can be performed on total cellular RNA or poly(A)+ mRNA. The preferred method of RNA analysis of the present invention is the use of total cellular RNA as described in other examples herein. Methods of RNA isolation are well known in the art. Northern blot analysis is also routine in the art. Real-time quantitative (PCR) can be conveniently accomplished using the commercially available ABI PRISM™ 7600, 7700, or 7900 Sequence Detection System, available from PE-Applied Biosystems, Foster City, CA and used according to manufacturer's instructions.

Protein levels of apolipoprotein C-III can be quantitated in a variety of ways well known in the art, such as immunoprecipitation, Western blot analysis (immunoblotting), enzyme-linked immunosorbent assay (ELISA) or fluorescence-activated cell sorting (FACS). Antibodies directed to apolipoprotein C-III can be identified and obtained from a variety of sources, such as the MSRS catalog

of antibodies (Aerie Corporation, Birmingham, MI), or can be prepared via conventional monoclonal or polyclonal antibody generation methods well known in the art.

Example 11: Design of phenotypic assays and *in vivo* studies for the use of apolipoprotein C-III inhibitors

Phenotypic assays

Once apolipoprotein C-III inhibitors have been identified by the methods disclosed herein, the compounds are further investigated in one or more phenotypic assays, each having measurable endpoints predictive of efficacy in the treatment of a particular disease state or condition. Phenotypic assays, kits and reagents for their use are well known to those skilled in the art and are herein used to investigate the role and/or association of apolipoprotein C-III in health and disease. Representative phenotypic assays, which can be purchased from any one of several commercial vendors, include those for determining cell viability, cytotoxicity, proliferation or cell survival (Molecular Probes, Eugene, OR; PerkinElmer, Boston, MA), protein-based assays including enzymatic assays (Panvera, LLC, Madison, WI; BD Biosciences, Franklin Lakes, NJ; Oncogene Research Products, San Diego, CA), cell regulation, signal transduction, inflammation, oxidative processes and apoptosis (Assay Designs Inc., Ann Arbor, MI), triglyceride accumulation (Sigma-Aldrich, St. Louis, MO), angiogenesis assays, tube formation assays, cytokine and hormone assays and metabolic assays (Chemicon International Inc., Temecula, CA; Amersham Biosciences, Piscataway, NJ).

In one non-limiting example, cells determined to be appropriate for a particular phenotypic assay (i.e., MCF-7 cells selected for breast cancer studies; adipocytes for

obesity studies) are treated with apolipoprotein C-III inhibitors identified from the *in vitro* studies as well as control compounds at optimal concentrations which are determined by the methods described above. At the end of the treatment period, treated and untreated cells are analyzed by one or more methods specific for the assay to determine phenotypic outcomes and endpoints.

Phenotypic endpoints include changes in cell morphology over time or treatment dose as well as changes in levels of cellular components such as proteins, lipids, nucleic acids, hormones, saccharides or metals. Measurements of cellular status, which include pH, stage of the cell cycle, intake or excretion of biological indicators by the cell, are also endpoints of interest.

Analysis of the genotype of the cell (measurement of the expression of one or more of the genes of the cell) after treatment is also used as an indicator of the efficacy or potency of the apolipoprotein C-III inhibitors. Hallmark genes, or those genes suspected to be associated with a specific disease state, condition, or phenotype, are measured in both treated and untreated cells.

In vivo studies

The individual subjects of the *in vivo* studies described herein are warm-blooded vertebrate animals, which includes humans.

The clinical trial is subjected to rigorous controls to ensure that individuals are not unnecessarily put at risk and that they are fully informed about their role in the study. To account for the psychological effects of receiving treatments, volunteers are randomly given placebo or apolipoprotein C-III inhibitor. Furthermore, to prevent

the doctors from being biased in treatments, they are not informed as to whether the medication they are administering is a apolipoprotein C-III inhibitor or a placebo. Using this randomization approach, each volunteer has the same chance of being given either the new treatment or the placebo.

Volunteers receive either the apolipoprotein C-III inhibitor or placebo for eight week period with biological parameters associated with the indicated disease state or condition being measured at the beginning (baseline measurements before any treatment), end (after the final treatment), and at regular intervals during the study period. Such measurements include the levels of nucleic acid molecules encoding apolipoprotein C-III or the levels of apolipoprotein C-III protein in body fluids, tissues or organs compared to pre-treatment levels. Other measurements include, but are not limited to, indices of the disease state or condition being treated, body weight, blood pressure, serum titers of pharmacologic indicators of disease or toxicity as well as ADME (absorption, distribution, metabolism and excretion) measurements.

Information recorded for each patient includes age (years), gender, height (cm), family history of disease state or condition (yes/no), motivation rating (some/moderate/great) and number and type of previous treatment regimens for the indicated disease or condition.

Volunteers taking part in this study are healthy adults (age 18 to 65 years) and roughly an equal number of males and females participate in the study. Volunteers with certain characteristics are equally distributed for placebo and apolipoprotein C-III inhibitor treatment. In general,

the volunteers treated with placebo have little or no response to treatment, whereas the volunteers treated with the apolipoprotein C-III inhibitor show positive trends in their disease state or condition index at the conclusion of the study.

Example 12: RNA Isolation

Poly(A)+ mRNA isolation

Poly(A)+ mRNA was isolated according to Miura *et al.*, (*Clin. Chem.*, **1996**, *42*, 1758-1764). Other methods for poly(A)+ mRNA isolation are routine in the art. Briefly, for cells grown on 96-well plates, growth medium was removed from the cells and each well was washed with 200 µL cold PBS. 60 µL lysis buffer (10 mM Tris-HCl, pH 7.6, 1 mM EDTA, 0.5 M NaCl, 0.5% NP-40, 20 mM vanadyl-ribonucleoside complex) was added to each well, the plate was gently agitated and then incubated at room temperature for five minutes. 55 µL of lysate was transferred to Oligo d(T) coated 96-well plates (AGCT Inc., Irvine CA). Plates were incubated for 60 minutes at room temperature, washed 3 times with 200 µL of wash buffer (10 mM Tris-HCl pH 7.6, 1 mM EDTA, 0.3 M NaCl). After the final wash, the plate was blotted on paper towels to remove excess wash buffer and then air-dried for 5 minutes. 60 µL of elution buffer (5 mM Tris-HCl pH 7.6), preheated to 70°C, was added to each well, the plate was incubated on a 90°C hot plate for 5 minutes, and the eluate was then transferred to a fresh 96-well plate.

Cells grown on 100 mm or other standard plates may be treated similarly, using appropriate volumes of all solutions.

Total RNA Isolation

Total RNA was isolated using an RNEASY 96™ kit and buffers purchased from Qiagen Inc. (Valencia, CA) following the manufacturer's recommended procedures. Briefly, for cells grown on 96-well plates, growth medium was removed from the cells and each well was washed with 200 µL cold PBS. 150 µL Buffer RLT was added to each well and the plate vigorously agitated for 20 seconds. 150 µL of 70% ethanol was then added to each well and the contents mixed by pipetting three times up and down. The samples were then transferred to the RNEASY 96™ well plate attached to a QIAVAC™ manifold fitted with a waste collection tray and attached to a vacuum source. Vacuum was applied for 1 minute. 500 µL of Buffer RW1 was added to each well of the RNEASY 96™ plate and incubated for 15 minutes and the vacuum was again applied for 1 minute. An additional 500 µL of Buffer RW1 was added to each well of the RNEASY 96™ plate and the vacuum was applied for 2 minutes. 1 mL of Buffer RPE was then added to each well of the RNEASY 96™ plate and the vacuum applied for a period of 90 seconds. The Buffer RPE wash was then repeated and the vacuum was applied for an additional 3 minutes. The plate was then removed from the QIAVAC™ manifold and blotted dry on paper towels. The plate was then re-attached to the QIAVAC™ manifold fitted with a collection tube rack containing 1.2 mL collection tubes. RNA was then eluted by pipetting 140 µL of RNAse free water into each well, incubating 1 minute, and then applying the vacuum for 3 minutes.

The repetitive pipetting and elution steps may be automated using a QIAGEN® Bio-Robot™ 9604 apparatus (Qiagen, Inc., Valencia CA). Essentially, after lysing of the cells

on the culture plate, the plate is transferred to the robot deck where the pipetting, DNase treatment and elution steps are carried out.

Example 13: Real-time Quantitative PCR Analysis of apolipoprotein C-III mRNA Levels

Quantitation of apolipoprotein C-III mRNA levels was accomplished by real-time quantitative PCR using the ABI PRISM™ 7600, 7700, or 7900 Sequence Detection System (PE-Applied Biosystems, Foster City, CA) according to manufacturer's instructions. This is a closed-tube, non-gel-based, fluorescence detection system which allows high-throughput quantitation of polymerase chain reaction (PCR) products in real-time. As opposed to standard PCR in which amplification products are quantitated after the PCR is completed, products in real-time quantitative PCR are quantitated as they accumulate. This is accomplished by including in the PCR reaction an oligonucleotide probe that anneals specifically between the forward and reverse PCR primers, and contains two fluorescent dyes. A reporter dye (e.g., FAM or JOE, obtained from either PE-Applied Biosystems, Foster City, CA, Operon Technologies Inc., Alameda, CA or Integrated DNA Technologies Inc., Coralville, IA) is attached to the 5' end of the probe and a quencher dye (e.g., TAMRA, obtained from either PE-Applied Biosystems, Foster City, CA, Operon Technologies Inc., Alameda, CA or Integrated DNA Technologies Inc., Coralville, IA) is attached to the 3' end of the probe. When the probe and dyes are intact, reporter dye emission is quenched by the proximity of the 3' quencher dye. During amplification, annealing of the probe to the target sequence creates a substrate that can be cleaved by the 5'-exonuclease activity

of Taq polymerase. During the extension phase of the PCR amplification cycle, cleavage of the probe by Taq polymerase releases the reporter dye from the remainder of the probe (and hence from the quencher moiety) and a sequence-specific fluorescent signal is generated. With each cycle, additional reporter dye molecules are cleaved from their respective probes, and the fluorescence intensity is monitored at regular intervals by laser optics built into the ABI PRISM™ Sequence Detection System. In each assay, a series of parallel reactions containing serial dilutions of mRNA from untreated control samples generates a standard curve that is used to quantitate the percent inhibition after antisense oligonucleotide treatment of test samples.

Prior to quantitative PCR analysis, primer-probe sets specific to the target gene being measured are evaluated for their ability to be "multiplexed" with a GAPDH amplification reaction. In multiplexing, both the target gene and the internal standard gene GAPDH are amplified concurrently in a single sample. In this analysis, mRNA isolated from untreated cells is serially diluted. Each dilution is amplified in the presence of primer-probe sets specific for GAPDH only, target gene only ("single-plexing"), or both (multiplexing). Following PCR amplification, standard curves of GAPDH and target mRNA signal as a function of dilution are generated from both the single-plexed and multiplexed samples. If both the slope and correlation coefficient of the GAPDH and target signals generated from the multiplexed samples fall within 10% of their corresponding values generated from the single-plexed samples, the primer-probe set specific for that target is deemed multiplexable. Other methods of PCR are also known in the art.

PCR reagents were obtained from Invitrogen Corporation, (Carlsbad, CA). RT-PCR reactions were carried out by adding 20 µL PCR cocktail (2.5x PCR buffer minus $MgCl_2$, 6.6 mM $MgCl_2$, 375 µM each of dATP, dCTP, dCTP and dGTP, 375 nM each of forward primer and reverse primer, 125 nM of probe, 4 Units RNAse inhibitor, 1.25 Units PLATINUM® Taq, 5 Units MuLV reverse transcriptase, and 2.5x ROX dye) to 96-well plates containing 30 µL total RNA solution (20-200 ng). The RT reaction was carried out by incubation for 30 minutes at 48°C. Following a 10 minute incubation at 95°C to activate the PLATINUM® Taq, 40 cycles of a two-step PCR protocol were carried out: 95°C for 15 seconds (denaturation) followed by 60°C for 1.5 minutes (annealing/extension).

Gene target quantities obtained by real time RT-PCR are normalized using either the expression level of GAPDH, a gene whose expression is constant, or by quantifying total RNA using RiboGreen™ reagent (Molecular Probes, Inc. Eugene, OR). GAPDH expression is quantified by real time RT-PCR, by being run simultaneously with the target, multiplexing, or separately. Total RNA is quantified using RiboGreen™ RNA quantification reagent (Molecular Probes, Inc. Eugene, OR). Methods of RNA quantification by RiboGreen™ reagent are taught in Jones, L.J., *et al.*, (Analytical Biochemistry, 1998, 265, 368-374).

In this assay, 170 µL of RiboGreen™ working reagent (RiboGreen™ reagent diluted 1:350 in 10mM Tris-HCl, 1 mM EDTA, pH 7.5) is pipetted into a 96-well plate containing 30 µL purified, cellular RNA. The plate is read in a CytoFluor 4000 reader (PE Applied Biosystems) with excitation at 485nm and emission at 530nm.

Probes and primers to human apolipoprotein C-III were designed to hybridize to a human apolipoprotein C-III sequence, using published sequence information (nucleotides 6238608 to 6242565 of the sequence with GenBank accession number NT_035088.1, incorporated herein as SEQ ID NO: 4). For human apolipoprotein C-III the PCR primers were: forward primer: TCAGCTTCATGCAGGGTTACAT (SEQ ID NO: 5) reverse primer: ACGCTGCTCAGTGCATCCT (SEQ ID NO: 6) and the PCR probe was: FAM-AAGCACGCCACCAAGACCGCC-TAMRA (SEQ ID NO: 7) where FAM is the fluorescent dye and TAMRA is the quencher dye. For human GAPDH the PCR primers were: forward primer: GAAGGTGAAGGTCGGAGTC(SEQ ID NO: 8) reverse primer: GAAGATGGTGATGGGATTTC GGGTCTCGCTCCTGGAAGAT(SEQ ID NO: 9) and the PCR probe was: 5' JOE-CAAGCTTCCCGTTCTCAGCC- TAMRA 3' (SEQ ID NO: 10) where JOE is the fluorescent reporter dye and TAMRA is the quencher dye.

Probes and primers to mouse apolipoprotein C-III were designed to hybridize to a mouse apolipoprotein C-III sequence, using published sequence information (GenBank accession number L04150.1, incorporated herein as SEQ ID NO: 11). For mouse apolipoprotein C-III the PCR primers were: forward primer: TGCAGGGCTACATGGAACAA (SEQ ID NO: 12) reverse primer: CGGACTCCTGCACGCTACTT (SEQ ID NO: 13) and the PCR probe was: FAM-CTCCAAGACGGTCCAGGATGCGC-TAMRA (SEQ ID NO: 14) where FAM is the fluorescent reporter dye and TAMRA is the quencher dye. For mouse GAPDH the PCR primers were: forward primer: GGCAAATTCAACGGCACAGT(SEQ ID NO: 15) reverse primer: GGGTCTCGCTCCTGGAAGAT(SEQ ID NO: 16) and the

PCR probe was: 5' JOE-AAGGCCGAGAATGGGAAGCTTGTCATC- TAMRA 3' (SEQ ID NO: 17) where JOE is the fluorescent reporter dye and TAMRA is the quencher dye.

Example 14: Northern blot analysis of apolipoprotein C-III mRNA levels

Eighteen hours after antisense treatment, cell monolayers were washed twice with cold PBS and lysed in 1 mL RNAZOL™ reagent(TEL-TEST "B" Inc., Friendswood, TX). Total RNA was prepared following manufacturer's recommended protocols. Twenty micrograms of total RNA was fractionated by electrophoresis through 1.2% agarose gels containing 1.1% formaldehyde using a MOPS buffer system (AMRESCO, Inc. Solon, OH). RNA was transferred from the gel to HYBOND™-N+ nylon membranes (Amersham Pharmacia Biotech, Piscataway, NJ) by overnight capillary transfer using a Northern/Southern Transfer buffer system (TEL-TEST "B" Inc., Friendswood, TX). RNA transfer was confirmed by UV visualization. Membranes were fixed by UV cross-linking using a STRATALINKER™ UV Crosslinker 2400 (Stratagene, Inc, La Jolla, CA) and then probed using QUICKHYB™ hybridization solution (Stratagene, La Jolla, CA) using manufacturer's recommendations for stringent conditions.

To detect human apolipoprotein C-III, a human apolipoprotein C-III specific probe was prepared by PCR using the forward primer TCAGCTTCATGCAGGGTTACAT (SEQ ID NO: 5) and the reverse primer ACGCTGCTCAGTGCATCCT (SEQ ID NO: 6). To normalize for variations in loading and transfer efficiency membranes were stripped and probed for human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) RNA (Clontech, Palo Alto, CA).

To detect mouse apolipoprotein C-III, a mouse apolipoprotein C-III specific probe was prepared by PCR using the forward primer TGCAGGGCTACATGGAACAA (SEQ ID NO: 12) and the reverse primer CGGACTCCTGCACGCTACTT (SEQ ID NO: 13). To normalize for variations in loading and transfer efficiency membranes were stripped and probed for mouse glyceraldehyde-3-phosphate dehydrogenase (GAPDH) RNA (Clontech, Palo Alto, CA).

Hybridized membranes were visualized and quantitated using a PHOSPHORIMAGER™ apparatus and IMAGEQUANT™ Software V3.3 (Molecular Dynamics, Sunnyvale, CA). Data was normalized to GAPDH levels in untreated controls.

Example 15: Antisense inhibition of human apolipoprotein C-III expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

In accordance with the present invention, a series of antisense compounds was designed to target different regions of the human apolipoprotein C-III RNA, using published sequences (nucleotides 6238608 to 6242565 of GenBank accession number NT_035088.1, representing a genomic sequence, incorporated herein as SEQ ID NO: 4, and GenBank accession number NM_000040.1, incorporated herein as SEQ ID NO: 18). The compounds are shown in Table 1. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds. All compounds in Table 1 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of *2'-O-(2-methoxyethyl) nucleotides*, also known as (2'-

MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines. The compounds were analyzed for their effect on human apolipoprotein C-III mRNA levels by quantitative real-time PCR as described in other examples herein. Data are averages from three experiments in which HepG2 cells were treated with the antisense oligonucleotides of the present invention. The positive control for each datapoint is identified in the table by sequence ID number. If present, "N.D." indicates "no data".

Table 1 - Inhibition of human apolipoprotein C-III mRNA levels by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

ISIS #	REGION	TARGET SEQ ID NO	TARGET SITE	SEQUENCE	% INHIB	SEQ ID NO	CONTROL SEQ ID NO
167824	5'UTR	4	414	ctggagcagctgcctctagg	79	19	1
167835	Coding	4	1292	ccctgcatgaagctgagaag	60	20	1
167837	Coding	18	141	gtgcttcatgtaaccctgca	88	21	1
167846	Coding	4	1369	tggcctgctgggccacctgg	66	22	1
167848	Coding	4	3278	tgctccagtagtctttcagg	81	23	1
167851	Coding	4	3326	tgacctcagggtccaaatcc	41	24	1
304739	5'UTR	4	401	ctctagggatgaactgagca	62	25	1
304740	5'UTR	4	408	cagctgcctctagggatgaa	44	26	1
304741	5'UTR	18	17	ttcctggagcagctgcctct	57	27	1
304742	5'UTR	18	24	acctctgttcctggagcagc	78	28	1
304743	Start Codon	18	29	atggcacctctgttcctgga	78	29	1
304744	Start Codon	4	1065	gggctgcatggcacctctgt	73	30	1
304745	Coding	4	1086	ggcaacaacaaggagtaccc	90	31	1
304746	Coding	4	1090	ggagggcaacaacaaggagt	80	32	1
304747	Coding	18	87	agctcgggcagaggccagga	49	33	1
304748	Coding	18	92	tctgaagctcgggcagaggc	72	34	1
304749	Coding	18	97	cggcctctgaagctcgggca	11	35	1
304750	Coding	4	1267	catcctcggcctctgaagct	49	36	1
304751	Coding	4	1273	gggaggcatcctcggcctct	65	37	1
304752	Coding	4	1278	gagaagggaggcatcctcgg	82	38	1
304753	Coding	4	1281	gctgagaagggaggcatcct	75	39	1
304754	Coding	4	1289	tgcatgaagctgagaaggga	74	40	1

304755	Coding	18	143	gcgtgcttcatgtaaccctg	95	41	1
304756	Coding	4	1313	ttggtggcgtgcttcatgta	92	42	1
304757	Coding	4	1328	gcatccttggcggtcttggt	98	43	1
304758	Coding	4	1334	ctcagtgcatccttggcggt	97	44	1
304759	Coding	4	1336	tgctcagtgcatccttggcg	93	45	1
304760	Coding	4	1347	ctcctgcacgctgctcagtg	65	46	1
304761	Coding	4	1349	gactcctgcacgctgctcag	77	47	1
304762	Coding	4	1358	gccacctgggactcctgcac	89	48	1
304763	Coding	18	210	gcccctggcctgctgggcca	71	49	1
304764	Coding	18	211	agcccctggcctgctgggcc	62	50	1
304765	Coding	4	3253	gaagccatcggtcacccagc	71	51	1
304766	Coding	4	3255	ctgaagccatcggtcaccca	85	52	1
304767	Coding	4	3265	tttcagggaactgaagccat	73	53	1
304768	Coding	4	3273	cagtagtctttcagggaact	40	54	1
304769	Coding	4	3283	aacggtgctccagtagtctt	66	55	1
304770	Coding	4	3287	ccttaacggtgctccagtag	88	56	1
304771	Coding	4	3295	gaacttgtccttaacggtgc	59	57	1
304772	Coding	4	3301	ctcagagaacttgtccttaa	88	58	1
304773	Coding	4	3305	agaactcagagaacttgtcc	75	59	1
304774	Coding	4	3310	atcccagaactcagagaact	0	60	1
304775	Coding	4	3320	cagggtccaaatcccagaac	70	61	1
304776	Coding	4	3332	ttggtctgacctcagggtcc	90	62	1
304777	Coding	4	3333	gttggtctgacctcagggtc	84	63	1
304778	Coding	4	3339	gctgaagttggtctgacctc	81	64	1
304779	Coding	4	3347	cagccacggctgaagttggt	75	65	1
304780	Stop Codon	4	3351	caggcagccacggctgaagt	83	66	1
304781	Stop Codon	4	3361	attgaggtctcaggcagcca	79	67	1
304782	3'UTR	4	3385	tggataggcaggtggacttg	64	68	1
304783	3'UTR	18	369	ctcgcaggatggataggcag	76	69	1
304784	3'UTR	18	374	aggagctcgcaggatggata	58	70	1
304785	3'UTR	18	380	gacccaaggagctcgcagga	73	71	1
304786	3'UTR	18	385	tgcaggacccaaggagctcg	92	72	1
304787	3'UTR	4	3417	tggagattgcaggacccaag	88	73	1
304788	3'UTR	4	3422	agccctggagattgcaggac	69	74	1
304789	3'UTR	4	3425	ggcagccctggagattgcag	76	75	1
304790	3'UTR	4	3445	ccttttaagcaacctacagg	65	76	1
304791	3'UTR	4	3450	ctgtcccttttaagcaacct	53	77	1
304792	3'UTR	4	3456	agaatactgtcccttttaag	72	78	1
304793	3'UTR	4	3461	cactgagaatactgtccctt	67	79	1
304794	3'UTR	4	3469	taggagagcactgagaatac	59	80	1
304795	3'UTR	4	3472	gggtaggagagcactgagaa	74	81	1
304796	3'UTR	4	3509	aggccagcatgcctggaggg	63	82	1
304797	3'UTR	4	3514	ttgggaggccagcatgcctg	55	83	1
304798	3'UTR	4	3521	agctttattgggaggccagc	90	84	1
304799	3'UTR	4	3526	tgtccagctttattgggagg	85	85	1
304800	3'UTR	4	3528	cttgtccagctttattggga	94	86	1
304801	3'UTR	4	3533	agcttcttgtccagctttat	74	87	1
304802	3'UTR	4	3539	catagcagcttcttgtccag	73	88	1
304803	exon:intron junction	4	416	acctggagcagctgcctcta	87	89	1
304804	exon:intron junction	4	424	agggcattacctggagcagc	68	90	1
304805	intron:exon junction	4	1053	acctctgttcctgcaaggaa	74	91	1
304806	exon:intron junction	4	1121	aagtgcttacgggcagaggc	78	92	1

304807	exon:intron junction	4	1380	gcgggtgtacctggcctgct	52	93	1
304808	intron	4	2337	aaccctgttgtgaactgcac	59	94	1
304809	intron	4	2405	agtgagcaataccgcctgag	80	95	1
304810	intron	4	2542	cgggcttgaattaggtcagg	56	96	1

As shown in Table 1, SEQ ID NOs 19, 20, 21, 22, 23, 25, 27, 28, 29, 30, 31, 32, 33, 34, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 55, 56, 57, 58, 59, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95 and 96 demonstrated at least 45% inhibition of human apolipoprotein C-III expression in this assay and are therefore preferred. More preferred are SEQ ID NOs 75, 86 and 85. The target regions to which these preferred sequences are complementary are herein referred to as "preferred target segments" and are therefore preferred for targeting by compounds of the present invention. These preferred target segments are shown in Table 3. The sequences represent the reverse complement of the preferred antisense compounds shown in Table 1. "Target site" indicates the first (5'-most) nucleotide number on the particular target nucleic acid to which the oligonucleotide binds. Also shown in Table 3 is the species in which each of the preferred target segments was found.

Example 16: Antisense inhibition of mouse apolipoprotein C-III expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap.

In accordance with the present invention, a second series of antisense compounds was designed to target different regions of the mouse apolipoprotein C-III RNA, using published sequences (GenBank accession number L04150.1, incorporated herein as SEQ ID NO: 11). The compounds are shown in Table 2. "Target site" indicates the

first (5'-most) nucleotide number on the particular target nucleic acid to which the compound binds. All compounds in Table 2 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of *2'-O-(2-methoxyethyl)nucleotides*, also known as (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines. The compounds were analyzed for their effect on mouse apolipoprotein C-III mRNA levels by quantitative real-time PCR as described in other examples herein. Data are averages from three experiments in which mouse primary hepatocyte cells were treated with the antisense oligonucleotides of the present invention. If present, "N.D." indicates "no data".

Table 2 - Inhibition of mouse apolipoprotein C-III mRNA levels by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

ISIS #	REGION	TARGET SEQ ID NO	TARGET SITE	SEQUENCE	% INHIB	SEQ ID NO
167858	5'UTR	11	1	tagggataaaactgagcagg	47	97
167859	5'UTR	11	21	ctggagtagctagctgcttc	30	98
167860	start codon	11	41	gctgcatggcacctacgtac	80	99
167861	coding	11	62	ccacagtgaggagcgtccgg	86	100
167862	coding	11	88	ggcagatgccaggagagcca	55	101
167863	coding	11	104	ctacctcttcagctcgggca	56	102
167864	coding	11	121	cagcagcaaggatccctcta	83	103
167865	coding	11	131	gcacagagcccagcagcaag	49	104
167867	coding	11	215	ccctggccaccgcagctata	67	105
167868	coding	11	239	atctgaagtgattgtccatc	11	106
167869	coding	11	254	agtagcctttcaggaatctg	57	107
167870	coding	11	274	cttgtcagtaaacttgctcc	89	108
167871	coding	11	286	gaagccggtgaacttgtcag	55	109
167872	coding	11	294	gaatcccagaagccggtgaa	29	110
167873	coding	11	299	ggttagaatcccagaagccg	55	111

167874	coding	11	319	tggagttggttggtcctcag	79	112
167875	stop codon	11	334	tcacgactcaatagctggag	77	113
167877	3'UTR	11	421	cccttaaagcaaccttcagg	71	114
167878	3'UTR	11	441	agacatgagaacatactttc	81	115
167879	3'UTR	11	471	catgtttaggtgagatctag	87	116
167880	3'UTR	11	496	tcttatccagctttattagg	98	117

As shown in Table 2, SEQ ID NOs 97, 99, 100, 101, 102, 103, 104, 105, 107, 108, 109, 111, 112, 113, 114, 115, 116 and 117 demonstrated at least 45% inhibition of mouse apolipoprotein C-III expression in this experiment and are therefore preferred. More preferred are SEQ ID NOs 117, 116, and 100. The target regions to which these preferred sequences are complementary are herein referred to as "preferred target segments" and are therefore preferred for targeting by compounds of the present invention. These preferred target segments are shown in Table 3. The sequences represent the reverse complement of the preferred antisense compounds shown in Table 2. These sequences are shown to contain thymine (T) but one of skill in the art will appreciate that thymine (T) is generally replaced by uracil (U) in RNA sequences. "Target site" indicates the first (5'-most) nucleotide number on the particular target nucleic acid to which the oligonucleotide binds. Also shown in Table 3 is the species in which each of the preferred target segments was found.

Table 3 - Sequence and position of preferred target segments identified in apolipoprotein C-III.

SITE ID	TARGET SEQ ID NO	TARGET SITE	SEQUENCE	REV COMP OF SEQ ID	ACTIVE IN	SEQ ID NO
82975	4	414	cctagaggcagctgctccag	19	*H. sapiens*	118
82980	4	1292	cttctcagcttcatgcaggg	20	*H. sapiens*	119
82981	18	141	tgcagggttacatgaagcac	21	*H. sapiens*	120
82985	4	1369	ccaggtggcccagcaggcca	22	*H. sapiens*	121

82987	4	3278	cctgaaagactactggagca	23	*H. sapiens*	122
220510	4	401	tgctcagttcatccctagag	25	*H. sapiens*	123
220512	18	17	agaggcagctgctccaggaa	27	*H. sapiens*	124
220513	18	24	gctgctccaggaacagaggt	28	*H. sapiens*	125
220514	18	29	tccaggaacagaggtgccat	29	*H. sapiens*	126
220515	4	1065	acagaggtgccatgcagccc	30	*H. sapiens*	127
220516	4	1086	gggtactccttgttgttgcc	31	*H. sapiens*	128
220517	4	1090	actccttgttgttgccctcc	32	*H. sapiens*	129
220518	18	87	tcctggcctctgcccgagct	33	*H. sapiens*	130
220519	18	92	gcctctgcccgagcttcaga	34	*H. sapiens*	131
220521	4	1267	agcttcagaggccgaggatg	36	*H. sapiens*	132
220522	4	1273	agaggccgaggatgcctccc	37	*H. sapiens*	133
220523	4	1278	ccgaggatgcctcccttctc	38	*H. sapiens*	134
220524	4	1281	aggatgcctcccttctcagc	39	*H. sapiens*	135
220525	4	1289	tcccttctcagcttcatgca	40	*H. sapiens*	136
220526	18	143	cagggttacatgaagcacgc	41	*H. sapiens*	137
220527	4	1313	tacatgaagcacgccaccaa	42	*H. sapiens*	138
220528	4	1328	accaagaccgccaaggatgc	43	*H. sapiens*	139
220529	4	1334	accgccaaggatgcactgag	44	*H. sapiens*	140
220530	4	1336	cgccaaggatgcactgagca	45	*H. sapiens*	141
220531	4	1347	cactgagcagcgtgcaggag	46	*H. sapiens*	142
220532	4	1349	ctgagcagcgtgcaggagtc	47	*H. sapiens*	143
220533	4	1358	gtgcaggagtcccaggtggc	48	*H. sapiens*	144
220534	18	210	tggcccagcaggccaggggc	49	*H. sapiens*	145
220535	18	211	ggcccagcaggccaggggct	50	*H. sapiens*	146
220536	4	3253	gctgggtgaccgatggcttc	51	*H. sapiens*	147
220537	4	3255	tgggtgaccgatggcttcag	52	*H. sapiens*	148
220538	4	3265	atggcttcagttccctgaaa	53	*H. sapiens*	149
220540	4	3283	aagactactggagcaccgtt	55	*H. sapiens*	150
220541	4	3287	ctactggagcaccgttaagg	56	*H. sapiens*	151
220542	4	3295	gcaccgttaaggacaagttc	57	*H. sapiens*	152
220543	4	3301	ttaaggacaagttctctgag	58	*H. sapiens*	153
220544	4	3305	ggacaagttctctgagttct	59	*H. sapiens*	154
220546	4	3320	gttctgggatttggaccctg	61	*H. sapiens*	155
220547	4	3332	ggaccctgaggtcagaccaa	62	*H. sapiens*	156
220548	4	3333	gaccctgaggtcagaccaac	63	*H. sapiens*	157
220549	4	3339	gaggtcagaccaacttcagc	64	*H. sapiens*	158
220550	4	3347	accaacttcagccgtggctg	65	*H. sapiens*	159
220551	4	3351	acttcagccgtggctgcctg	66	*H. sapiens*	160
220552	4	3361	tggctgcctgagacctcaat	67	*H. sapiens*	161
220553	4	3385	caagtccacctgcctatcca	68	*H. sapiens*	162
220554	18	369	ctgcctatccatcctgcgag	69	*H. sapiens*	163
220555	18	374	tatccatcctgcgagctcct	70	*H. sapiens*	164
220556	18	380	tcctgcgagctccttgggtc	71	*H. sapiens*	165
220557	18	385	cgagctccttgggtcctgca	72	*H. sapiens*	166
220558	4	3417	cttgggtcctgcaatctcca	73	*H. sapiens*	167
220559	4	3422	gtcctgcaatctccagggct	74	*H. sapiens*	168
220560	4	3425	ctgcaatctccagggctgcc	75	*H. sapiens*	169
220561	4	3445	cctgtaggttgcttaaaagg	76	*H. sapiens*	170
220562	4	3450	aggttgcttaaaagggacag	77	*H. sapiens*	171
220563	4	3456	cttaaaagggacagtattct	78	*H. sapiens*	172
220564	4	3461	aagggacagtattctcagtg	79	*H. sapiens*	173
220565	4	3469	gtattctcagtgctctccta	80	*H. sapiens*	174
220566	4	3472	ttctcagtgctctcctaccc	81	*H. sapiens*	175
220567	4	3509	ccctccaggcatgctggcct	82	*H. sapiens*	176
220568	4	3514	caggcatgctggcctcccaa	83	*H. sapiens*	177

220569	4	3521	gctggcctcccaataaagct	84	*H. sapiens*	178
220570	4	3526	cctcccaataaagctggaca	85	*H. sapiens*	179
220571	4	3528	tcccaataaagctggacaag	86	*H. sapiens*	180
220572	4	3533	ataaagctggacaagaagct	87	*H. sapiens*	181
220573	4	3539	ctggacaagaagctgctatg	88	*H. sapiens*	182
220574	4	416	tagaggcagctgctccaggt	89	*H. sapiens*	183
220575	4	424	gctgctccaggtaatgccct	90	*H. sapiens*	184
220576	4	1053	ttccttgcaggaacagaggt	91	*H. sapiens*	185
220577	4	1121	gcctctgcccgtaagcactt	92	*H. sapiens*	186
220578	4	1380	agcaggccaggtacacccgc	93	*H. sapiens*	187
220579	4	2337	gtgcagttcacaacagggtt	94	*H. sapiens*	188
220580	4	2405	ctcaggcggtattgctcact	95	*H. sapiens*	189
220581	4	2542	cctgacctaattcaagcccg	96	*H. sapiens*	190
82997	11	1	cctgctcagttttatcccta	97	*M. musculus*	191
82999	11	41	gtacgtaggtgccatgcagc	99	*M. musculus*	192
83000	11	62	ccggacgctcctcactgtgg	100	*M. musculus*	193
83001	11	88	tggctctcctggcatctgcc	101	*M. musculus*	194
83002	11	104	tgcccgagctgaagaggtag	102	*M. musculus*	195
83003	11	121	tagagggatccttgctgctg	103	*M. musculus*	196
83004	11	131	cttgctgctgggctctgtgc	104	*M. musculus*	197
83006	11	215	tatagctgcggtggccaggg	105	*M. musculus*	198
83008	11	254	cagattcctgaaaggctact	107	*M. musculus*	199
83009	11	274	ggagcaagtttactgacaag	108	*M. musculus*	200
83010	11	286	ctgacaagttcaccggcttc	109	*M. musculus*	201
83012	11	299	cggcttctgggattctaacc	111	*M. musculus*	202
83013	11	319	ctgaggaccaaccaactcca	112	*M. musculus*	203
83014	11	334	ctccagctattgagtcgtga	113	*M. musculus*	204
83016	11	421	cctgaaggttgctttaaggg	114	*M. musculus*	205
83017	11	441	gaaagtatgttctcatgtct	115	*M. musculus*	206
83018	11	471	ctagatctcacctaaacatg	116	*M. musculus*	207
83019	11	496	cctaataaagctggataaga	117	*M. musculus*	208

As these "preferred target segments" have been found by experimentation to be open to, and accessible for, hybridization with the antisense compounds of the present invention, one of skill in the art will recognize or be able to ascertain, using no more than routine experimentation, further embodiments of the invention that encompass other compounds that specifically hybridize to these preferred target segments and consequently inhibit the expression of apolipoprotein C-III.

According to the present invention, antisense compounds include antisense oligomeric compounds, antisense oligonucleotides, ribozymes, external guide sequence (EGS) oligonucleotides, alternate splicers, primers, probes, and

other short oligomeric compounds that hybridize to at least a portion of the target nucleic acid.

Example 17: Antisense inhibition of human apolipoprotein C-III expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap - additional antisense compounds

In accordance with the present invention, an additional series of antisense compounds was designed to target different regions of the human apolipoprotein C-III RNA, using published sequences (nucleotides 6238608 to 6242565 of the sequence with GenBank accession number NT_035088.1, representing a genomic sequence, incorporated herein as SEQ ID NO: 4, and GenBank accession number NM_000040.1, incorporated herein as SEQ ID NO: 18). The compounds are shown in Table 4. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds. All compounds in Table 4 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of *2'-O-(2-methoxyethyl)nucleotides*, also known as (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines. The compounds were analyzed for their effect on human apolipoprotein C-III mRNA levels by quantitative real-time PCR as described in other examples herein. Data are averages from three experiments in which

HepG2 cells were treated with the antisense oligonucleotides of the present invention. If present, "N.D." indicates "no data".

Table 4 - Inhibition of human apolipoprotein C-III mRNA levels by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

ISIS #	TARGET SEQ ID NO	TARGET SITE	SEQUENCE	% INHIB	SEQ ID NO
167826	4	1063	gctgcatggcacctctgttc	0	209
167828	4	1110	ggcagaggccaggagcgcca	0	210
167830	18	91	ctgaagctcgggcagaggcc	9	211
167832	18	101	tcctcggcctctgaagctcg	0	212
167840	4	1315	tcttggtggcgtgcttcatg	0	213
167842	4	1335	gctcagtgcatccttggcgg	38	214
167844	4	1345	cctgcacgctgctcagtgca	28	215
167847	4	3256	actgaagccatcggtcaccc	0	216
167850	4	3306	cagaactcagagaacttgtc	0	217
167852	4	3336	gaagttggtctgacctcagg	0	218
167853	4	3420	ccctggagattgcaggaccc	0	219
167854	4	3426	gggcagccctggagattgca	22	220
167855	4	3446	ccctttaagcaacctacag	27	221

Example 18: Antisense inhibition of human apolipoprotein C-III expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap: dose-response study in HepG2 cells

In accordance with the present invention, a subset of the antisense oligonucleotides from Examples 15 and 17 was further investigated in a dose-response study. Treatment doses of ISIS 167842 (SEQ ID NO: 214), ISIS 167844 (SEQ ID NO: 215), ISIS 167846 (SEQ ID NO: 22), ISIS 167837 (SEQ ID NO: 21), ISIS 304789 (SEQ ID NO: 75), ISIS 304799 (SEQ ID NO: 85), and ISIS 304800 (SEQ ID: 86) were 50, 150 and 300 nM. The compounds were analyzed for their effect on human apolipoprotein C-III mRNA levels in HepG2 cells by

quantitative real-time PCR as described in other examples herein. Data are averages from two experiments and are shown in Table 5.

Table 5 - Inhibition of human apolipoprotein C-III mRNA levels by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

ISIS #	SEQ ID NO	Dose of oligonucleotide		
		50 nM	150 nM	300 nM
		Percent Inhibition		
167842	214	88	77	92
167844	215	86	86	84
167846	22	79	80	79
167837	21	83	86	84
304789	75	81	91	92
304799	85	82	93	88
304800	86	80	86	91

These data demonstrate that the expression of apolipoprotein C-III is inhibited in a dose-dependent manner upon treatment of cells with antisense compounds targeting apolipoprotein C-III. These compounds were further analyzed in Hep3B cells for their ability to reduce mRNA levels in Hep3B cells and it was determined that ISIS 167842 and 167837 inhibited apolipoprotein C-III expression in a dose dependent manner in this cell line as well.

Example 19: Antisense inhibition mouse apolipoprotein C-III expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap- dose-response study in primary mouse hepatocytes

In accordance with the present invention, a subset of the antisense oligonucleotides in Example 16 was further investigated in dose-response studies. Treatment doses with

ISIS 167861 (SEQ ID NO: 100), ISIS 167870 (SEQ ID NO: 108), ISIS 167879 (SEQ ID NO: 116), and ISIS 167880 (SEQ ID NO: 117) were 40, 120 and 240 nM. The compounds were analyzed for their effect on mouse apolipoprotein C-III mRNA levels in primary hepatocyte cells by quantitative real-time PCR as described in other examples herein. Data are averages from two experiments and are shown in Table 6.

Table 6 - Inhibition of mouse apolipoprotein C-III mRNA levels by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap - dose-response study

		Dose of oligonucleotide		
ISIS #	SEQ ID NO	40 nM	120 nM	240 nM
		Percent Inhibition		
167861	100	48	49	61
167870	108	16	16	46
167879	116	25	54	81
167880	117	76	81	93

These data demonstrate that the expression of mouse apolipoprotein C-III can be inhibited in a dose-dependent manner by treatment with antisense compounds.

Example 20: Western blot analysis of apolipoprotein C-III protein levels

Western blot analysis (immunoblot analysis) is carried out using standard methods. Cells are harvested 16-20 h after oligonucleotide treatment, washed once with PBS, suspended in Laemmli buffer (100 µl/well), boiled for 5 minutes and loaded on a 16% SDS-PAGE gel. Gels are run for 1.5 hours at 150 V, and transferred to membrane for western blotting. Appropriate primary antibody directed to apolipoprotein C-III is used, with a radiolabelled or fluorescently labeled secondary antibody directed against

the primary antibody species. Bands are visualized using a PHOSPHORIMAGER™ instrument (Molecular Dynamics, Sunnyvale CA).

Example 21: Effects of antisense inhibition of apolipoprotein C-III (ISIS 167880) on serum cholesterol and triglyceride levels

C57BL/6 mice, a strain reported to be susceptible to hyperlipidemia-induced atherosclerotic plaque formation were used in the following studies to evaluate apolipoprotein C-III antisense oligonucleotides as potential agents to lower cholesterol and triglyceride levels.

Male C57BL/6 mice (n=8) receiving a high fat diet (60% kcal fat) were evaluated over the course of 6 weeks for the effects of ISIS 167880 (SEQ ID NO: 117) on serum cholesterol and triglyceride levels. Control animals received saline treatment. Mice were dosed intraperitoneally every three days (twice a week), after fasting overnight, with 50 mg/kg ISIS 167880 or saline for six weeks.

Male C57BL/6 mice fed a normal rodent diet were fasted overnight then dosed intraperitoneally every three days with saline (control), 50 mg/kg ISIS 167880 (SEQ ID NO: 117) or 50 mg/kg ISIS 167879 (SEQ ID NO: 116) for two weeks.

At study termination, forty eight hours after the final injections, the animals were sacrificed and evaluated for serum cholesterol and triglyceride levels and compared to the saline control. Measurements of serum cholesterol and triglyceride levels were obtained through routine clinical analysis.

High fat fed mice treated with ISIS 167880 showed a reduction in both serum cholesterol (196 mg/dL for control animals and 137 mg/dL for ISIS 167880) and triglycerides

(151 mg/dL for control animals and 58 mg/dL for ISIS 167880) by study end.

No effect was seen on serum cholesterol levels for lean mice treated with ISIS 167880 (91 mg/dL for control animals and 91 mg/dL for ISIS 167880), however triglycerides were lowered (91 mg/dL for control animals and 59 mg/dL for ISIS 167880) by study end.

Lean mice treated with ISIS 167879 showed an increase in serum cholesterol (91 mg/dL for control animals and 116 mg/dL for ISIS 167879) but a reduction in triglycerides (91 mg/dL for control animals and 65 mg/dL for ISIS 167879) by study end.

These results indicate that, in mice fed a high fat diet, ISIS 167880 reduces cholesterol and triglyceride to levels that are comparable to lean littermates while having no deleterious effects on the lean animals. (See Table 7 for summary of *in vivo* data.)

Example 22: Effects of antisense inhibition of apolipoprotein C-III (ISIS 167880) on serum AST and ALT levels

C57BL/6 mice were used in the following studies to evaluate the liver toxicity of apolipoprotein C-III antisense oligonucleotides.

Male C57BL/6 mice (n=8) receiving a high fat diet (60% kcal fat) were evaluated over the course of 6 weeks for the effects of ISIS 167880 (SEQ ID NO: 117) on liver enzyme (AST and ALT) levels. Control animals received saline treatment. Mice were dosed intraperitoneally every three days (twice a week), after fasting overnight, with 50 mg/kg ISIS 167880 or saline for six weeks.

Male C57BL/6 mice fed a normal rodent diet were fasted overnight then dosed intraperitoneally every three days with saline (control), 50 mg/kg ISIS 167880 (SEQ ID NO: 117) or 50 mg/kg ISIS 167879 (SEQ ID NO: 116) for two weeks.

At study termination and forty-eight hours after the final injections, animals were sacrificed and evaluated for serum AST and ALT levels, which were measured by routine clinical methods. Increased levels of the liver enzymes ALT and AST can indicate toxicity and liver damage.

High fat fed mice treated with ISIS 167880 showed an increase in AST levels over the duration of the study compared to saline controls (157 IU/L for ISIS 167880, compared to 92 IU/L for saline control).

ALT levels in high fat fed mice were increased by treatments with ISIS 167880 over the duration of the study compared to saline controls (64 IU/L for ISIS 167880, compared to 40 IU/L for saline control).

Lean mice treated with ISIS 167880 showed no significant increase in AST and ALT levels over the duration of the study compared to saline controls (AST levels of 51 IU/L for control compared to 58 IU/L for ISIS 167880; ALT levels of 26 IU/L for control compared to 27 IU/L for ISIS 167880).

Lean mice treated with ISIS 167879 showed no change in AST levels and a decrease in ALT levels over the duration of the study compared to saline controls (AST levels of 51 IU/L for control compared to 51 IU/L for ISIS 167879; ALT levels of 26 IU/L for control compared to 21 IU/L for ISIS 167879).

These results suggest a minor liver toxicity effect from ISIS 167880 in mice fed a high fat diet but no liver toxicity from ISIS 167880 or 167879 in mice fed a normal rodent diet. (See Table 7 for summary of *in vivo* data.)

Example 23: Effects of antisense inhibition of apolipoprotein C-III (ISIS 167880) on serum glucose levels

Male C57BL/6 mice (n=8) receiving a high fat diet (60% kcal fat) were evaluated over the course of 6 weeks for the effects of ISIS 167880 (SEQ ID NO: 117) on serum glucose levels. Control animals received saline treatment. Mice were dosed intraperitoneally every three days (twice a week), after fasting overnight, with 50 mg/kg ISIS 167880 or saline for six weeks.

Male C57BL/6 mice fed a normal rodent diet were fasted overnight then dosed intraperitoneally every three days with saline (control), 50 mg/kg ISIS 167880 (SEQ ID NO: 117) or 50 mg/kg ISIS 167879 (SEQ ID NO: 116) for two weeks.

At study termination and forty-eight hours after the final injections, animals were sacrificed and evaluated for serum glucose levels, which was measured by routine clinical methods.

In the high fat fed mice, ISIS 167880 reduced serum glucose levels to 183 mg/dL, compared to the saline control of 213 mg/dL. In lean mice, ISIS 167880 had no significant effect on serum glucose levels with measurements of 203 mg/dL, compared to the saline control of 204 mg/dL; while ISIS 167879 only slightly increased serum glucose levels to 216 mg/dL.

These results indicate that, in mice fed a high fat diet, ISIS 167880 is able to reduce serum glucose to levels comparable to lean littermates, while having no deleterious effects on the lean animals. (See Table 7 for summary of *in vivo* data.)

Example 24: Effects of antisense inhibition of apolipoprotein C-III (ISIS 167880) on apolipoprotein C-III mRNA levels in C57BL/6 mice

Male C57BL/6 mice received a high fat diet (60% kcal fat) fasted overnight, and dosed intraperitoneally every three days with saline or 50 mg/kg ISIS 167880 (SEQ ID NO: 117) for six weeks.

Male C57BL/6 mice fed a normal rodent diet were fasted overnight then dosed intraperitoneally every three days with saline (control) or 50 mg/kg ISIS 167880 (SEQ ID NO: 117) or 50 mg/kg ISIS 167879 (SEQ ID NO: 116) for two weeks.

At study termination, forty-eight hours after the final injections, animals were sacrificed and evaluated for apolipoprotein C-III mRNA levels in liver. The high fat fed mice dosed with ISIS 167880 had apolipoprotein C-III mRNA levels 8% that of the saline treated mice. The lean mice showed decreased apolipoprotein C-III mRNA after treatment with either ISIS 167880 or ISIS 167879. The lean mice dosed with ISIS 167880 had apolipoprotein C-III mRNA levels 21% that of the saline treated mice and those dosed with ISIS 167879 had apolipoprotein C-III mRNA levels 27% that of the saline treated mice.

These results indicate that in both high fat fed mice and lean mice, antisense oligonucleotides directed against apolipoprotein C-III are able to decrease apolipoprotein C-III mRNA levels *in vivo* to a similar extent. (See Table 7 for summary of *in vivo* data.)

Table 7 - Effects of ISIS 167880 or 167879 treatment on cholesterol, triglyceride, glucose, liver enzyme, and apolipoprotein C-III mRNA in liver, in lean and high fat fed C57BL/6 mice.

	Biological Marker Measured units	ISIS #	Diet, Experiment duration	
			High Fat, 6 week	Lean, 2 week
	Cholesterol mg/dL	control	196	91
		167880	137	91
		167879	N.D.	116
	Triglycerides mg/dL	control	151	91
		167880	58	59
		167879	N.D.	65
	Glucose mg/dL	control	213	204
		167880	183	203
		167879	N.D.	216
Liver Enzymes	AST IU/L	control	92	51
		167880	157	58
		167879	N.D.	51
	ALT IU/L	control	40	26
		167880	64	27
		167879	N.D.	21
	Apolipoprotein C-III mRNA % of control	167880	8%	21%
		167879	N.D.	27%

In summary, these results indicate that, in mice fed a high fat diet, ISIS 167880 is able to reduce serum glucose, cholesterol and triglyceride to levels comparable to lean littermates, while having no deleterious effects on the lean animals. Furthermore, antisense oligonucleotides directed against apolipoprotein C-III are able to decrease apolipoprotein C-III mRNA levels *in vivo* to a similar extent in both high fat fed mice and lean mice. These results suggest a minor liver toxicity effect from ISIS 167880 in mice fed a high fat diet but no liver toxicity from ISIS 167880 or 167879 in mice fed a normal rodent diet.

Example 25: Antisense inhibition of apolipoprotein C-III mRNA *in vivo*

C57BL/6 mice, a strain reported to be susceptible to hyperlipidemia-induced atherosclerotic plaque formation, were used in the following studies to evaluate apolipoprotein C-III antisense oligonucleotides as potential agents to lower cholesterol and triglyceride levels. Accordingly, in a further embodiment, C57BL/6 mice on a high-fat diet were treated with antisense oligonucleotides targeted to apolipoprotein C-III.

Male C57BL/6 mice (n=8; 7 to 8 weeks of age) receiving a high fat diet (60% kcal fat) were evaluated for apolipoprotein C-III mRNA expression in liver after 6 weeks of treatment with antisense oligonucleotides targeted to apolipoprotein C-III. Mice received twice weekly intraperitoneal injections at a dose of 25 mg/kg of ISIS 167880 (SEQ ID NO: 117), ISIS 167875 (SEQ ID NO: 113), ISIS 167878 (SEQ ID NO: 115) or ISIS 167879 (SEQ ID NO: 116). Control animals received saline treatment twice weekly for a period of 6 weeks.

At study termination, forty-eight hours after the final injections, the animals were sacrificed and evaluated for apolipoprotein C-III mRNA expression in liver. RNA was isolated from liver and mRNA was quantitated as described herein. Apolipoprotein C-III mRNA levels from each treatment group (n=8) were averaged. Relative to saline-treated animals, treatment with ISIS 167875, ISIS 167878, ISIS 167879 and ISIS 167880 resulted in a 24%, 56%, 50% and 77% reduction in apolipoprotein C-III mRNA levels,

respectively, demonstrating that these compounds significantly reduced apolipoprotein C-III mRNA expression in liver.

Example 26: Effects of antisense inhibition of apolipoprotein C-III on serum cholesterol, triglyceride, glucose and serum transaminases

In a further embodiment, the mice treated with saline or a 25 mg/kg dose of ISIS 167880 (SEQ ID NO: 117), ISIS 167875 (SEQ ID NO: 113), ISIS 167878 (SEQ ID NO: 115) or ISIS 167879 (SEQ ID NO: 116) as described in Example 25 were evaluated for serum cholesterol and triglyceride levels following 6 weeks of treatment.

At study termination, forty-eight hours after the dose of saline or antisense compound, the animals were sacrificed and evaluated for serum cholesterol, triglyceride and glucose levels by routine analysis using an Olympus Clinical Analyzer (Olympus America Inc., Melville, NY). The serum transaminases ALT and AST, increases in which can indicate hepatotoxicity, were also measured using an Olympus Clinical Analyzer (Olympus America Inc., Melville, NY). The levels of serum cholesterol, triglycerides and glucose are presented in Table 8 as the average result from each treatment group (n=8), in mg/dL. ALT and AST, also shown in Table 8, are also shown as the average result from each treatment group (n=8), in international units/L (IU/L).

Table 8 - Effects of antisense inhibition of apolipoprotein C-III on serum cholesterol, triglyceride, glucose and transaminases

	Treatment				
Serum marker	Saline	ISIS 167875	ISIS 167878	ISIS 167879	ISIS 167880
Total Cholesterol mg/dL	172	197	180	132	155
HDL Cholesterol mg/dL	149	162	157	117	137
LDL Cholesterol mg/dL	25	37	28	24	21
Serum Triglyerides mg/dL	126	99	75	60	52
ALT IU/L	24	555	32	45	66
AST IU/L	56	489	76	117	132
Glucose mg/dL	273	234	251	189	255

A significant reduction in serum triglyceride levels was observed following treatment with ISIS 167875, ISIS 167878, ISIS 167879 and ISIS 167880, which reduced triglyercide levels 22%, 40%, 52% and 58%, respectively. This reduction in serum triglycerides correlated with the reduction in apolipoprotein C-III liver mRNA expression. Moreover, reductions in target and serum triglycerides following treatment with ISIS 167878, ISIS 167879 and ISIS 167880 were not accompanied by hepatoxicity, as indicated by the lack of significant increases in ALT and AST levels. Glucose levels were significantly lowered following treatment with ISIS 167879.

Example 27: Effects of antisense inhibition of apolipoprotein C-III on body weight and organ weight

In a further embodiment, the animals treated with saline or a 25 mg/kg dose of ISIS 167880 (SEQ ID NO: 117), ISIS 167875 (SEQ ID NO: 113), ISIS 167878 (SEQ ID NO: 115) or ISIS 167879 (SEQ ID NO: 116) as described in Example 25 were evaluated for changes in body weight, fat pad, liver and spleen weights. At study termination, forty-eight hours following the final dose of saline or antisense compound, the animals were sacrificed and body and organ weights were measured. The data shown in Table 9 represent average weights from all animals in each treatment group (n=8). Body weight is presented in grams (g), while spleen, liver and fat pad weights are presented in milligrams (mg).

Table 9 - Effects of antisense inhibition of apolipoprotein C-III on body and organ weights

	Treatment				
	Saline	ISIS 167875	ISIS 167878	ISIS 167879	ISIS 167880
Body weight (g)	33	30	32	28	30
Liver weight (mg)	126	190	141	133	146
Fat pad weight (mg)	182	125	125	61	62
Spleen weight (mg)	8	12	12	12	14

As is evident in Table 9, treatment with antisense compounds targeted to mouse apolipoprotein C-III resulted in significant reductions in fat pad weight. ISIS 167875 and ISIS 167878 both led to a 31% reduction in fat pad weight, while ISIS 167879 and ISIS 167880 both resulted in a 66% lowering of fat pad weight. Body weights were not significantly changed and spleen weights were slightly

increased following antisense compound treatment. With the exception livers from animals treated with ISIS 167875, liver weights were not significantly changed.

Example 28: Effects of antisense inhibition of apolipoprotein C-III on liver triglyceride levels

Hepatic steatosis refers to the accumulation of lipids in the liver, or "fatty liver", which is frequently caused by alcohol consumption, diabetes and hyperlipidemia and can progress to end-stage liver damage. Given the deleterious consequences of a fatty liver condition, it is of use to identify compounds that prevent or ameliorate hepatic steatosis. Hepatic steatosis is evaluated both by measurement of tissue triglyceride content and by histologic examination of liver tissue.

In a further embodiment, liver tissue triglyceride content was assessed in the animals treated with saline or a 25 mg/kg dose of ISIS 167880 (SEQ ID NO: 117), ISIS 167875 (SEQ ID NO: 113), ISIS 167878 (SEQ ID NO: 115) or ISIS 167879 (SEQ ID NO: 116) as described in Example 25. Liver tissue triglyceride content was measured using the Triglyceride GPO assay (Roche Diagnostics, Indianapolis, IN). Histological analysis was conducted by routine procedures, whereby liver tissue was fixed in neutral-buffered formalin, embedded in paraffin, sectioned and subsequently stained with hematoxylin and eosin, to visualize nuclei and cytoplasm, respectively. Alternatively, liver tissue was procured then immediately frozen, sectioned, and subsequently stained with oil red O stain to visualize lipid deposits and counterstained with eosin to mark cytoplasm. The prepared samples were evaluated by light microscopy.

Relative to saline treated mice, liver tissue triglyceride levels were significantly lowered, by 25%, 35%, 40% and 64% following treatment with ISIS 167875, ISIS 167878, ISIS 167879 and ISIS 167880, respectively. Histological analysis of stained liver sections similarly revealed a reduction in liver tissue triglycerides. Thus, as demonstrated by measurement of tissue triglycerides and histological analyses of liver tissue sections, treatment with antisense compounds targeted to apolipoprotein C-III reduced liver triglyceride content. As such, antisense compounds targeted to apolipoprotein C-III are candidate therapeutic agents for the prevention or amelioration of hepatic steatosis.

Example 29: Antisense inhibition of apolipoprotein C-III in Cynomolgus monkey primary hepatocytes

In a further embodiment, antisense compounds targeted to human apolipoprotein C-III were tested for their effects on apolipoprotein C-III expression in primary Cynomolgus monkey hepatocytes. Pre-plated primary Cynomolgus monkey hepatocytes were purchased from InVitro Technologies (Baltimore, MD). Cells were cultured in high-glucose DMEM (Invitrogen Life Technologies, Carlsbad, CA) supplemented with 10% fetal bovine serum (Invitrogen Life Technologies, Carlsbad, CA), 100 units/mL and 100 μg/mL streptomycin (Invitrogen Life Technologies, Carlsbad, CA).

Cells at a density of 80,000 cells per well in a 24-well plate were treated with 10, 50, 150 and 300 nM of ISIS 304789 (SEQ ID NO: 75), ISIS 304799 (SEQ ID NO: 85) or ISIS 304800 (SEQ ID NO: 86). ISIS 113529 (CTCTTACTGTGCTGTGGACA, SEQ ID NO: 222) served as a control oligonucleotide. ISIS 113529 is a chimeric oligonucleotide ("gapmer") 20

nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of *2'-O-(2-methoxyethyl)nucleotides*, also known as (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines.

Following 24 hours of treatment with antisense oligonucleotides, apolipoprotein C-III mRNA was measured by real-time PCR as described by other examples herein, using the primers and probe designed to the human apolipoprotein C-III sequence (SEQ ID NOs 5, 6 and 7) to measure Cynomolgous monkey apolipoprotein C-III mRNA. Primers and probe designed to human GAPDH (SEQ ID NOs 8, 9 and 10) were used to measure Cynomolgous monkey GAPDH mRNA expression, for the purpose of normalizing gene target quantities obtained by real-time PCR. Untreated cells served as the control to which data were normalized. Data are the average of three experiments and are presented in Table 10.

Table 10 - Antisense inhibition of apolipoprotein C-III in Cynomolgus monkey primary hepatocytes

ISIS #	SEQ ID NO	Dose of Oligonucleotide			
		10 nM	50 nM	150 nM	300 nM
		% Inhibition			
304789	75	0	7	1	55
304799	85	34	60	66	48
304800	86	9	53	59	57
113529	222	N.D.	N.D.	0	0

Example 30: Cynomolgus monkey apolipoprotein C-III sequence

In a further embodiment, a portion of the Cynomolgus monkey apolipoprotein C-III gene was sequenced. Positions 8 to 476 of the human apolipoprotein C-III mRNA sequence (incorporated in its entirety herein as SEQ ID NO: 18) contain the target segment to which ISIS 304789 hybridizes. The corresponding region of Cynomolgus monkey apolipoprotein C-III mRNA was sequenced. RNA was isolated and purified from primary Cynomolgus monkey hepatocytes (InVitro Technologies, Gaithersburg, MD) and was subjected to a reverse transcriptase reaction (kit from Invitrogen Life Technologies, Carlsbad, CA). The resultant cDNA was the substrate for 40 rounds of PCR amplification, using 5′ and 3′ primers designed to positions 8 and 476, respectively, of the human apolipoprotein C-III mRNA (Amplitaq PCR kit, Invitrogen Life Technologies, Carlsbad, CA). Following gel purification of the resultant 468 bp fragment, the forward and reverse sequencing reactions of each product were performed by Retrogen (San Diego, CA). This Cynomolgus monkey sequence is incorporated herein as SEQ ID NO: 223 and is 92% identical to positions 8 to 476 of the human apolipoprotein C-III mRNA.

Example 31: Chimeric phosphorothioate oligonucleotide having 2′-MOE wings and a deoxy gap, targeted to Cynomolgus monkey apolipoprotein C-III

In a further embodiment, the sequence of Cynomolgus monkey apolipoprotein C-III incorporated herein as SEQ ID NO: 223 was used to design an antisense oligonucleotide having 100% complementarity to Cynomolgus apolipoprotein C-III mRNA. ISIS 340340 (GGCAGCCCTGGAGGCTGCAG; incorporated herein as SEQ ID NO: 224) targets nucleotide 397 of SEQ ID

NO: 223, within a region corresponding to the 3′ UTR of the human apolipoprotein C-III to which ISIS 304789 hybridizes. ISIS 340340 is a chimeric oligonucleotide ("gapmer") 20 nucleotide in length composed of a central "gap" region consisting of 2′deoxynucleotides, which is flanked on both sides (5′ and 3′ directions) by 5 nucleotide "wings". The wings are composed of 2′methoxyethyl (2′-MOE) nucleotides. Internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the nucleotide. All cytidine residues are 5-methyl cytidines.

Example 32: Antisense inhibition of rat apolipoprotein C-III expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

In a further embodiment, for the purpose of designing antisense oligonucleotides to both coding and untranslated regions of rat apolipoprotein C-III mRNA, a segment of rat apolipoprotein C-III mRNA was sequenced to provide 3′ UTR sequence, as the published rat apolipoprotein C-III mRNA sequence is restricted to the coding region. RNA was isolated and purified from primary rat hepatocytes (InVitro Technologies, Gaithersburg, MD) and was subjected to a reverse transcriptase reaction (kit from Invitrogen Life Technologies, Carlsbad, CA). The resultant cDNA was the substrate for 40 rounds of PCR amplification (Amplitaq PCR kit, Invitrogen Life Technologies, Carlsbad, CA), using forward and reverse primers that anneal to the 5′-most and 3′-most ends, respectively, of mouse apolipoprotein C-III mRNA. Following gel purification of the resultant 427 bp fragment, the forward and reverse sequencing reactions of each product were performed by Retrogen (San Diego, CA). This rat sequence is incorporated herein as SEQ ID NO: 225

and includes an additional 121 bp in the 3′ direction from the stop codon of apolipoprotein C-III, with respect to the published sequence (GenBank accession number NM_012501.1, incorporated herein as SEQ ID NO: 226).

A series of antisense compounds was designed to target different regions of the rat apolipoprotein C-III mRNA, using SEQ ID NO: 225. The compounds are shown in Table 11. "Target site" indicates the first (5′-most) nucleotide number on the particular target sequence to which the compound binds. All compounds in Table 11 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of *2′-O-(2-methoxyethyl)nucleotides*, also known as (2′-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines.

The compounds were analyzed for their effect on rat apolipoprotein C-III mRNA levels by quantitative real-time PCR as described in other examples herein. Probes and primers to rat apolipoprotein C-III were designed to hybridize to a rat apolipoprotein C-III sequence, using published sequence information (GenBank accession number NM_012501.1, incorporated herein as SEQ ID NO: 226). For rat apolipoprotein C-III the PCR primers were:
forward primer: GAGGGAGAGGGATCCTTGCT (SEQ ID NO: 227)
reverse primer: GGACCGTCTTGGAGGCTTG (SEQ ID NO: 228)
and the PCR probe was: FAM-CTGGGCTCTATGCAGGGCTACATGGA-TAMRA, SEQ ID NO: 229) where FAM is the fluorescent dye and TAMRA is the quencher dye. For rat GAPDH the PCR primers were:

forward primer: TGTTCTAGAGACAGCCGCATCTT (SEQ ID NO: 230) reverse primer: CACCGACCTTCACCATCTTGT (SEQ ID NO: 231) and the PCR probe was JOE-TTGTGCAGTGCCAGCCTCGTCTCA-TAMRA (SEQ ID NO: 232) where JOE is the fluorescent reporter dye and TAMRA is the quencher dye.

Data are from an experiment in which primary rat hepatocytes were treated with 150 nM of the antisense oligonucleotides of the invention. Results, shown in Table 11, are expressed as percent inhibition relative to untreated control cells. If present, "N.D." indicates "no data".

Table 11 - Antisense inhibition of rat apolipoprotein C-III mRNA levels by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

ISIS #	REGION	TARGET SEQ ID NO	TARGET SITE	SEQUENCE	% INHIB	SEQ ID NO
340982	Coding	225	213	TGAACTTATCAGTGAACTTG	0	233
340987	Coding	225	238	TCAGGGCCAGACTCCCAGAG	7	234
340988	Coding	225	258	TTGGTGTTGTTAGTTGGTCC	0	235
340991	Coding	225	258	TTGGTGTTGTTAGTTGGTCC	0	236
353932	Coding	225	10	AGAGCCACGAGGGCCACGAT	0	237
353933	Coding	225	20	AGAGGCCAGGAGAGCCACGA	15	238
353934	Coding	225	30	CAGCTCGGGCAGAGGCCAGG	2	239
353935	Coding	225	40	TCTCCCTCATCAGCTCGGGC	0	240
353936	Coding	225	59	GCCCAGCAGCAAGGATCCCT	73	241
353937	Coding	225	69	CCTGCATAGAGCCCAGCAGC	0	242
353938	Coding	225	79	TCCATGTAGCCCTGCATAGA	90	243
353940	Coding	225	99	GGACCGTCTTGGAGGCTTGT	76	244
353941	Coding	225	109	AGTGCATCCTGGACCGTCTT	61	245
353942	Coding	225	119	CATGCTGCTTAGTGCATCCT	0	246
353943	Coding	225	129	CAGACTCCTGCATGCTGCTT	57	247
353944	Coding	225	139	ACAGCTATATCAGACTCCTG	0	248
353945	Coding	225	148	CTGGCCACCACAGCTATATC	0	249
353946	Coding	225	169	AAGCGATTGTCCATCCAGCC	0	250
353949	Coding	225	195	TGCTCCAGTAGCCTTTCAGG	0	251
353950	Coding	225	200	GAACTTGCTCCAGTAGCCTT	35	252
353951	Coding	225	204	CAGTGAACTTGCTCCAGTAG	0	253
353952	Coding	225	209	CTTATCAGTGAACTTGCTCC	0	254

353953	Coding	225	217	CCAGTGAACTTATCAGTGAA	0	255
353954	Coding	225	221	GAGGCCAGTGAACTTATCAG	0	256
353955	Coding	225	224	CCAGAGGCCAGTGAACTTAT	31	257
353956	Coding	225	229	GACTCCCAGAGGCCAGTGAA	0	258
353957	Coding	225	234	GGCCAGACTCCCAGAGGCCA	0	259
353958	Coding	225	247	AGTTGGTCCTCAGGGCCAGA	0	260
353959	Coding	225	250	GTTAGTTGGTCCTCAGGGCC	0	261
353960	Coding	225	254	TGTTGTTAGTTGGTCCTCAG	0	262
353961	Coding	225	262	AGAGTTGGTGTTGTTAGTTG	0	263
353962	Coding	225	267	GCTCAAGAGTTGGTGTTGTT	0	264
353963	Coding	225	271	CACGGCTCAAGAGTTGGTGT	0	265
353964	Stop Codon	225	275	GTCTCACGGCTCAAGAGTTG	0	266
353966	Stop Codon	225	285	GAACATGGAGGTCTCACGGC	55	267
353967	Stop Codon	225	289	TCTGGAACATGGAGGTCTCA	0	268
353968	3'UTR	225	293	CACATCTGGAACATGGAGGT	0	269
353969	3'UTR	225	297	CAGACACATCTGGAACATGG	0	270
353970	3'UTR	225	301	TGGCCAGACACATCTGGAAC	49	271
353972	3'UTR	225	309	AGGATAGATGGCCAGACACA	47	272
353973	3'UTR	225	313	CAGCAGGATAGATGGCCAGA	0	273
353974	3'UTR	225	317	GAGGCAGCAGGATAGATGGC	38	274
353975	3'UTR	225	321	TTCGGAGGCAGCAGGATAGA	0	275
353976	3'UTR	225	325	AACCTTCGGAGGCAGCAGGA	19	276
353977	3'UTR	225	329	GAGCAACCTTCGGAGGCAGC	88	277
353978	3'UTR	225	333	CTTAGAGCAACCTTCGGAGG	77	278
353979	3'UTR	225	337	TCCCCTTAGAGCAACCTTCG	0	279
353980	3'UTR	225	341	ACTTTCCCCTTAGAGCAACC	45	280
353981	3'UTR	225	345	ATATACTTTCCCCTTAGAGC	28	281
353982	3'UTR	225	349	GAGAATATACTTTCCCCTTA	96	282
353983	3'UTR	225	353	GCATGAGAATATACTTTCCC	69	283
353984	3'UTR	225	357	AAAGGCATGAGAATATACTT	47	284
353985	3'UTR	225	361	GGATAAAGGCATGAGAATAT	0	285
353986	3'UTR	225	365	GGAGGGATAAAGGCATGAGA	0	286
353987	3'UTR	225	386	GCATGTTTAGGTGAGGTCTG	100	287
353988	3'UTR	225	390	GACAGCATGTTTAGGTGAGG	0	288
353990	3'UTR	225	398	TTATTTGGGACAGCATGTTT	0	289
353991	3'UTR	225	402	GCTTTTATTTGGGACAGCAT	0	290
353992	3'UTR	225	407	TCCCAGCTTTTATTTGGGAC	22	291

In a further embodiment, an additional series of oligonucleotides was designed to target different regions of the rat apolipoprotein C-III RNA, using sequences described herein (SEQ ID NO: 225 and the sequence with Genbank accession number NM_012501.1, incorporated herein as SEQ ID NO: 226). The oligonucleotides are shown in Table 12. "Target site" indicates the first (5'-most) nucleotide

number on the particular target sequence to which the oligonucleotide binds. All compounds in Table 12 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of eight 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by 3-nucleotide "wings." The wings are composed of *2'-O-(2-methoxyethyl)nucleotides*, also known as (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines.

Table 12 - Chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap targeted to rat apolipoprotein C-III mRNA

ISIS #	REGION	TARGET SEQ ID NO	TARGET SITE	SEQUENCE	SEQ ID NO
340937	Coding	226	8	CACGATGAGGAGCATTCGGG	292
340938	Coding	226	13	AGGGCCACGATGAGGAGCAT	293
340939	Coding	225	6	CCACGAGGGCCACGATGAGG	294
340940	Coding	225	11	GAGAGCCACGAGGGCCACGA	295
340941	Coding	225	16	GCCAGGAGAGCCACGAGGGC	296
340942	Coding	225	21	CAGAGGCCAGGAGAGCCACG	297
340943	Coding	225	26	TCGGGCAGAGGCCAGGAGAG	298
340944	Coding	225	31	TCAGCTCGGGCAGAGGCCAG	299
340945	Coding	225	36	CCTCATCAGCTCGGGCAGAG	300
340946	Coding	225	41	CTCTCCCTCATCAGCTCGGG	301
340947	Coding	225	46	GATCCCTCTCCCTCATCAGC	302
340948	Coding	225	51	GCAAGGATCCCTCTCCCTCA	303
340949	Coding	225	56	CAGCAGCAAGGATCCCTCTC	304
340950	Coding	225	61	GAGCCCAGCAGCAAGGATCC	305
340951	Coding	225	66	GCATAGAGCCCAGCAGCAAG	306
340952	Coding	225	71	GCCCTGCATAGAGCCCAGCA	307
340953	Coding	225	76	ATGTAGCCCTGCATAGAGCC	308
340954	Coding	225	81	GTTCCATGTAGCCCTGCATA	309
340955	Coding	225	86	GGCTTGTTCCATGTAGCCCT	310
340956	Coding	225	91	TTGGAGGCTTGTTCCATGTA	311
340957	Coding	225	96	CCGTCTTGGAGGCTTGTTCC	312
340958	Coding	225	101	CTGGACCGTCTTGGAGGCTT	313

340959	Coding	225	106	GCATCCTGGACCGTCTTGGA	314
340960	Coding	225	111	TTAGTGCATCCTGGACCGTC	315
340961	Coding	225	116	GCTGCTTAGTGCATCCTGGA	316
340962	Coding	225	121	TGCATGCTGCTTAGTGCATC	317
340963	Coding	225	126	ACTCCTGCATGCTGCTTAGT	318
340964	Coding	225	131	ATCAGACTCCTGCATGCTGC	319
340965	Coding	225	136	GCTATATCAGACTCCTGCAT	320
340966	Coding	225	141	CCACAGCTATATCAGACTCC	321
340967	Coding	225	146	GGCCACCACAGCTATATCAG	322
340968	Coding	226	163	CTGCTGGCCACCACAGCTAT	323
340969	Coding	226	168	AGCCCCTGCTGGCCACCACA	324
340970	Coding	226	173	CATCCAGCCCCTGCTGGCCA	325
340971	Coding	226	178	TTGTCCATCCAGCCCCTGCT	326
340972	Coding	226	179	ATTGTCCATCCAGCCCCTGC	327
340973	Coding	225	168	AGCGATTGTCCATCCAGCCC	328
340974	Coding	225	173	TTTGAAGCGATTGTCCATCC	329
340975	Coding	225	178	AGGGATTTGAAGCGATTGTC	330
340976	Coding	225	183	CTTTCAGGGATTTGAAGCGA	331
340977	Coding	225	188	GTAGCCTTTCAGGGATTTGA	332
340978	Coding	225	193	CTCCAGTAGCCTTTCAGGGA	333
340979	Coding	225	198	ACTTGCTCCAGTAGCCTTTC	334
340980	Coding	225	203	AGTGAACTTGCTCCAGTAGC	335
340981	Coding	225	208	TTATCAGTGAACTTGCTCCA	336
340983	Coding	225	218	GCCAGTGAACTTATCAGTGA	337
340984	Coding	225	223	CAGAGGCCAGTGAACTTATC	338
340985	Coding	225	228	ACTCCCAGAGGCCAGTGAAC	339
340986	Coding	225	233	GCCAGACTCCCAGAGGCCAG	340
340989	Coding	225	248	TAGTTGGTCCTCAGGGCCAG	341
340990	Coding	225	253	GTTGTTAGTTGGTCCTCAGG	342
340992	Coding	225	263	AAGAGTTGGTGTTGTTAGTT	343
340993	Coding	225	268	GGCTCAAGAGTTGGTGTTGT	344
340994	Stop Codon	225	272	TCACGGCTCAAGAGTTGGTG	345
353939	Coding	225	89	GGAGGCTTGTTCCATGTAGC	346
353947	Coding	225	180	TCAGGGATTTGAAGCGATTG	347
353948	Coding	225	190	CAGTAGCCTTTCAGGGATTT	348
353965	Stop Codon	225	281	ATGGAGGTCTCACGGCTCAA	349
353971	3' UTR	225	305	TAGATGGCCAGACACATCTG	350
353989	3' UTR	225	394	TTGGGACAGCATGTTTAGGT	351

Example 33: Antisense inhibition of rat apolipoprotein C-III by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap: dose response study in primary rat hepatocytes

In a further embodiment, four oligonucleotides were selected for additional dose response studies. Primary rat hepatocytes were treated with 10, 50, 150, and 300 nM of ISIS 167878 (SEQ ID NO: 115), ISIS 167880 (SEQ ID NO: 117), ISIS 340982 (SEQ ID NO: 233), or the scrambled control oligo ISIS 113529 (SEQ ID NO: 222) and mRNA levels were measured 24 hours after oligonucleotide treatment as described in other examples herein. Untreated cells served as the control to which the data were normalized.

Results of these studies are shown in Table 13. Data are averages from three experiments and are expressed as percent inhibition, relative to untreated controls. Where present, "N.D." indicates "no data".

Table 13 - Antisense inhibition of apolipoprotein C-III mRNA expression in primary rat hepatocytes 24 hours after oligonucleotide treatment

		Dose of oligonucleotide			
ISIS #	SEQ ID NO	10 nM	50 nM	150 nM	300 nM
		% Inhibition			
167878	115	0	0	0	4
167880	117	21	19	20	33
340982	233	15	70	83	91
113529	222	N.D.	N.D.	N.D.	9

As shown in Table 13, ISIS 340982 was effective at reducing apolipoprotein C-III mRNA levels in a dose-dependent manner.

Example 34: Antisense inhibition of rat apolipoprotein C-III by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap: additional dose response study in primary rat hepatocytes

In a further embodiment, an additional group of antisense oligonucleotides targeted to rat apolipoprotein C-III was selected for dose response studies. Primary rat hepatocytes were treated with 10, 50, 150 and 300 nM of ISIS 353977 (SEQ ID NO: 277), ISIS 353978 (SEQ ID NO: 278), ISIS 353982 (SEQ ID NO: 282), ISIS 353983 (SEQ ID NO: 283), or ISIS 353987 (SEQ ID NO: 287) for a period of 24 hours. Target expression levels were quantitated by real-time PCR as described herein. Untreated cells served as the control to which data were normalized. The results, shown in Table 14, are the average of three experiments and are presented as percent inhibition of apolipoprotein C-III mRNA, relative to untreated control cells.

Table 14 - Dose-dependent inhibition of apolipoprotein C-III mRNA expression in primary rat hepatocytes 24 hours after oligonucleotide treatment

ISIS #	SEQ ID NO	Dose of oligonucleotide			
		10 nM	50 nM	150 nM	300 nM
		% Inhibition			
353977	277	26	10	3	2
353978	278	46	23	8	5
353982	282	35	21	10	2
353983	283	46	23	12	2
353987	287	38	25	12	4

These data demonstrate that ISIS 353977, ISIS 353978, ISIS 353982, ISIS 353983, and ISIS 353987 effectively reduce apolipoprotein C-III mRNA in a dose-dependent manner.

Example 35: Antisense inhibition of rat apolipoprotein C-III *in vivo*: mRNA levels

In a further embodiment, the effects of antisense inhibition of apolipoprotein C-III in rats were evaluated. Male Sprague-Dawley rats 6 weeks of age (Charles River Labs, Wilmington, MA) were fed a normal rodent diet. Animals received intraperitoneal injections of ISIS 340982 (SEQ ID NO: 233) twice weekly for two weeks. One group of animals (n= 4) received 75 mg/kg ISIS 340982 and one group of animals (n= 4) received 100 mg/kg ISIS 340982. Saline-treated animals (n = 4) served as a control group.

At the end of the treatment period, animals were sacrificed and RNA was isolated from liver. Apolipoprotein C-III mRNA was measured as described by other examples herein. Results from each treatment group were averaged and the mRNA levels in livers from ISIS 340982-treated mice were normalized to the mRNA levels in livers from saline-treated mice. Treatment with 75 mg/kg or 100 mg/kg ISIS 340982 resulted in a 69% reduction and an 84% reduction in liver apolipoprotein C-III mRNA, respectively, demonstrating that ISIS 340982 effectively inhibited target mRNA expression *in vivo*.

Example 36: Effects of antisense inhibition of rat apolipoprotein C-III *in vivo*: body, liver and spleen weights

In a further embodiment, the rats treated with ISIS 340782 (SEQ ID NO: 233) as described in Example 35 were assessed for changes in body, liver and spleen weights. Body weights were recorded at the initiation of the study (Week 0). Following the two-week treatment with twice-weekly injections of saline or ISIS 340782 at 75 or 100 mg/kg, animals were sacrificed, forty-eight hours after the

fourth and final injections, the animals were sacrificed. Body, liver and spleen weights were recorded at study termination.

Table 15 - Body, liver and spleen weights in rats treated with antisense oligonucleotide targeted to apolipoprotein C-III

Measurement	Saline		Treatment with ISIS 340892			
			75 mg/kg		100 mg/kg	
	Week 0	Week 2	Week 0	Week 2	Week 0	Week 2
Body weight (g)	529	536	485	448	478	425
Liver weight (g)	N.D.	19	N.D.	14	N.D.	16
Spleen weight (mg)	N.D.	1.1	N.D.	1.6	N.D.	1.6

These data demonstrate that antisense inhibition of apolipoprotein C-III mRNA was not associated with significant changes in body, liver or spleen weight.

Example 37: Effects of antisense inhibition of rat apolipoprotein C-III *in vivo*: blood lipids and glucose levels

In a further embodiment, the rats treated as described in Example 35 were evaluated for changes in blood total cholesterol, triglycerides, HDL-cholesterol, LDL-cholesterol, free fatty acids and glucose. Blood samples were collected just prior to the treatments (Week 0) and following the two week treatment with twice weekly injections of saline or ISIS 340982 (SEQ ID NO: 233) at 75 or 100 mg/kg. Total cholesterol, HDL-cholesterol, LDL-cholesterol, triglyceride, free fatty acid and glucose levels were measured by routine clinical methods using an Olympus Clinical Analyzer (Olympus America Inc., Melville, NY). Data from the four animals in each treatment group were averaged. The results are presented in Table 16.

Table 16 - Effects of antisense inhibition of rat apolipoprotein C-III on blood lipids and glucose

Biological Marker Measured	Treatment					
	Saline		75 mg/kg ISIS 340982		100 mg/kg ISIS 340982	
	Week 0	Week 2	Week 0	Week 2	Week 0	Week 2
Triglycerides Mg/dL	162	162	111	24	139	17
Total Cholesterol Mg/dL	112	102	106	40	107	31
HDL-Cholesterol Mg/dL	66	63	83	23	96	17
LDL-Cholesterol Mg/dL	29	32	35	13	37	10
Free Fatty Acids mEq/L	0.48	0.46	0.72	0.70	0.57	0.53
Glucose Mg/dL	153	151	147	127	164	166

From the data presented in Table 16 it is evident that ISIS 340982 treatment, at both doses administered, to significantly reduced circulating triglycerides, total cholesterol, HDL-cholesterol and LDL-cholesterol in rats. Furthermore, these animals exhibited reduced expression of apolipoprotein C-III mRNA in liver following treatment with ISIS 340982.

Example 38: Effects of antisense inhibition of rat apolipoprotein C-III *in vivo*: serum transaminases

In a further embodiment, the rats treated as described in Example 35 were evaluated for liver toxicity following antisense oligonucleotide treatment. Following the two week treatment with twice weekly injections of 75 mg/kg and 100 mg/kg ISIS 340982 (SEQ ID NO: 233), animals were sacrificed and blood was collected and processed for routine clinical analysis. The serum transaminases ALT and AST, increases in which can indicate hepatotoxicity, were also measured using

an Olympus Clinical Analyzer (Olympus America Inc., Melville, NY). ALT and AST levels, shown in Table 17, are shown as the average result from the 4 animals in each treatment group, in international units/L (IU/L).

Table 17 - Effects of treatment with ISIS 340982 on serum transaminase levels in rats

	Treatment		
Serum Transaminase	**Saline**	**75 mg/kg ISIS 340982**	**100 mg/kg ISIS 340982**
ALT IU/L	70	49	59
AST IU/L	93	127	147

ALT or AST levels twice that of the saline control are considered indicative of hepatotoxicity. These data demonstrate that ISIS 340982 treatment of rats, either at a dose of 75 mg/kg or 100 mg/kg, did not result in significant hepatotoxicity.

Example 39: Antisense inhibition of hamster apolipoprotein C-III expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

In a further embodiment, for the purpose of designing antisense oligonucleotides to different regions of hamster apolipoprotein C-III mRNA, a segment of *Mesocricetus auratus* hamster apolipoprotein C-III mRNA was sequenced to provide a segment of coding region and 3′ UTR sequence, as no published sequence of hamster apolipoprotein C-III mRNA was available. RNA was isolated and purified from primary hamster hepatocytes and was subjected to a reverse transcriptase reaction (kit from Invitrogen Life Technologies, Carlsbad, CA). The resultant cDNA was the

substrate for 40 rounds of PCR amplification (Amplitaq PCR kit, Invitrogen Life Technologies, Carlsbad, CA) using forward and reverse primers complementary to the 5′ and 3′ ends, respectively, of the mouse apolipoprotein C-III mRNA sequence. Following gel purification of the resultant 435 bp fragment, the forward and reverse sequencing reactions of each product were performed by Retrogen (San Diego, CA). This hamster sequence is incorporated herein as SEQ ID NO: 352.

A series of oligonucleotides was designed to target regions of the hamster apolipoprotein C-III mRNA (SEQ ID NO: 352). The oligonucleotides are shown in Table 18. "Target site" indicates the first (5′-most) nucleotide number on the particular target sequence to which the oligonucleotide binds. All compounds in Table 18 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings." The wings are composed of *2′-O-(2-methoxyethyl)nucleotides*, also known as (2′-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines.

The compounds were analyzed for their effect on hamster apolipoprotein C-III levels in primary hamster hepatocytes by quantitative real-time PCR as described in other examples herein. Probes and primers to hamster apolipoprotein C-III were designed to hybridize to a hamster apolipoprotein C-III sequence, using the hamster mRNA sequence described herein (SEQ ID NO: 352). For hamster apolipoprotein CIII the PCR primers were:

forward primer: CGCTAACCAGCATGCAAAAG (SEQ ID NO: 353)
reverse primer: CACCGTCCATCCAGTCCC(SEQ ID NO: 354) and the PCR probe was: FAM-CTGAGGTGGCTGTGCGGGCC-TAMRA (SEQ ID NO: 355) where FAM is the fluorescent dye and TAMRA is the quencher dye.

For hamster GAPDH the PCR primers were:
forward primer: CCAGCCTCGCTCCGG (SEQ ID NO: 356)
reverse primer: CCAATACGGCCAAATCCG (SEQ ID NO: 357)
and the PCR probe was JOE-ACGCAATGGTGAAGGTCGGCG-TAMRA (SEQ ID NO: 358) where JOE is the fluorescent reporter dye and TAMRA is the quencher dye.

Data are from an experiment in which primary hamster hepatocytes were treated with 150 nM of the oligonucleotides of the present invention. The data, shown in Table 18, are normalized to untreated control cells. If present, "N.D." indicates "no data."

Table 18 - Antisense inhibition of hamster apolipoprotein C-III mRNA levels by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

ISIS #	REGION	TARGET SEQ ID NO	TARGET SITE	SEQUENCE	% INHIB	SEQ ID NO
352929	Coding	352	5	TGCCAAGAGGGCAACAATAG	17	359
352930	Coding	352	10	AGGAGTGCCAAGAGGGCAAC	62	360
352931	Coding	352	16	GATGCCAGGAGTGCCAAGAG	50	361
352932	Coding	352	20	GGCAGATGCCAGGAGTGCCA	51	362
352933	Coding	352	39	CTCTACCTCATTAGCTTCGG	0	363
352934	Coding	352	41	CCCTCTACCTCATTAGCTTC	47	364
352935	Coding	352	44	GACCCCTCTACCTCATTAGC	0	365
352936	Coding	352	49	GCAAGGACCCCTCTACCTCA	15	366
352937	Coding	352	54	CAGCAGCAAGGACCCCTCTA	45	367
352938	Coding	352	59	GAGCCCAGCAGCAAGGACCC	0	368
352939	Coding	352	65	TGCACAGAGCCCAGCAGCAA	84	369
352940	Coding	352	70	AGCCCTGCACAGAGCCCAGC	0	370
352941	Coding	352	75	CATGTAGCCCTGCACAGAGC	0	371
352942	Coding	352	80	TGTTCCATGTAGCCCTGCAC	49	372

352943	Coding	352	85	TGGCCTGTTCCATGTAGCCC	55	373
352945	Coding	352	95	ACCTTCTTGGTGGCCTGTTC	62	374
352946	Coding	352	106	GCGCATCCTGGACCTTCTTG	0	375
352948	Coding	352	115	TGCTGGTTAGCGCATCCTGG	0	376
352949	Coding	352	120	TTGCATGCTGGTTAGCGCAT	3	377
352950	Coding	352	125	GACTTTTGCATGCTGGTTAG	59	378
352951	Coding	352	130	CCTCAGACTTTTGCATGCTG	72	379
352952	Coding	352	135	AGCCACCTCAGACTTTTGCA	75	380
352953	Coding	352	140	CGCACAGCCACCTCAGACTT	64	381
352955	Coding	352	153	CCAGTCCCTGGCCCGCACAG	66	382
352956	Coding	352	159	GTCCATCCAGTCCCTGGCCC	73	383
352957	Coding	352	161	CCGTCCATCCAGTCCCTGGC	0	384
352958	Coding	352	165	GCCACCGTCCATCCAGTCCC	0	385
352959	Coding	352	170	GTGAAGCCACCGTCCATCCA	12	386
352960	Coding	352	174	GGAGGTGAAGCCACCGTCCA	0	387
352961	Coding	352	193	TGCTCCAGTAGCTTTTCAGG	59	388
352962	Coding	352	200	GTAAATGTGCTCCAGTAGCT	66	389
352963	Coding	352	205	TGTCAGTAAATGTGCTCCAG	78	390
352965	Coding	352	214	TGGAGACCGTGTCAGTAAAT	38	391
352966	Coding	352	217	GGCTGGAGACCGTGTCAGTA	66	392
352967	Coding	352	221	CAGAGGCTGGAGACCGTGTC	13	393
352968	Coding	352	225	ATCCCAGAGGCTGGAGACCG	0	394
352969	Coding	352	230	GAAGAATCCCAGAGGCTGGA	54	395
352970	Coding	352	269	TCTCAAGGCTCAGTAGCTGG	0	396
352971	Coding	352	275	TAGAGGTCTCAAGGCTCAGT	70	397
352972	Stop Codon	352	280	GAACGTAGAGGTCTCAAGGC	61	398
352973	Stop Codon	352	286	CATTTGGAACGTAGAGGTCT	64	399
352974	3' UTR	352	292	CAAGCACATTTGGAACGTAG	0	400
352975	3' UTR	352	300	TGGACACACAAGCACATTTG	0	401
352976	3' UTR	352	305	CAGGATGGACACACAAGCAC	43	402
352977	3' UTR	352	311	GGCCAGCAGGATGGACACAC	81	403
352978	3' UTR	352	318	GCCCAGAGGCCAGCAGGATG	60	404
352979	3' UTR	352	348	CCTTTCAAACAACCTTCAGG	56	405
352980	3' UTR	352	402	GGACAGCATGTTTAGGTGAC	67	406

In a further embodiment, an additional series of oligonucleotides was designed to target different regions of the hamster apolipoprotein C-III RNA described herein (SEQ ID NO: 352). The oligonucleotides are shown in Table 19. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the oligonucleotide binds. All compounds in Table 19 are chimeric oligonucleotides ("gapmers") 20 nucleotides in

length, composed of a central "gap" region consisting of eight 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by 3-nucleotide "wings." The wings are composed of 2'-O-(2-methoxyethyl)nucleotides, also known as (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines.

Table 19 - Chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap targeted to hamster apolipoprotein C-III mRNA

ISIS #	REGION	TARGET SEQ ID NO	TARGET SITE	SEQUENCE	SEQ ID NO
352944	Coding	352	90	CTTGGTGGCCTGTTCCATGT	407
352947	Coding	352	110	GTTAGCGCATCCTGGACCTT	408
352954	Coding	352	145	TGGCCCGCACAGCCACCTCA	409
352964	Coding	352	210	GACCGTGTCAGTAAATGTGC	410
356295	Coding	352	1	AAGAGGGCAACAATAGGAGT	411
356296	Coding	352	6	GTGCCAAGAGGGCAACAATA	412
356297	Coding	352	15	ATGCCAGGAGTGCCAAGAGG	413
356298	Coding	352	25	CTTCGGGCAGATGCCAGGAG	414
356299	Coding	352	31	CATTAGCTTCGGGCAGATGC	415
356300	Coding	352	60	AGAGCCCAGCAGCAAGGACC	416
356301	Coding	352	86	GTGGCCTGTTCCATGTAGCC	417
356302	Coding	352	91	TCTTGGTGGCCTGTTCCATG	418
356303	Coding	352	96	GACCTTCTTGGTGGCCTGTT	419
356304	Coding	352	101	TCCTGGACCTTCTTGGTGGC	420
356305	Coding	352	111	GGTTAGCGCATCCTGGACCT	421
356306	Coding	352	116	ATGCTGGTTAGCGCATCCTG	422
356307	Coding	352	121	TTTGCATGCTGGTTAGCGCA	423
356308	Coding	352	126	AGACTTTTGCATGCTGGTTA	424
356309	Coding	352	131	ACCTCAGACTTTTGCATGCT	425
356310	Coding	352	136	CAGCCACCTCAGACTTTTGC	426
356311	Coding	352	141	CCGCACAGCCACCTCAGACT	427
356312	Coding	352	146	CTGGCCCGCACAGCCACCTC	428
356313	Coding	352	151	AGTCCCTGGCCCGCACAGCC	429
356314	Coding	352	156	CATCCAGTCCCTGGCCCGCA	430
356315	Coding	352	166	AGCCACCGTCCATCCAGTCC	431
356316	Coding	352	171	GGTGAAGCCACCGTCCATCC	432

356317	Coding	352	176	AGGGAGGTGAAGCCACCGTC	433
356318	Coding	352	181	TTTTCAGGGAGGTGAAGCCA	434
356319	Coding	352	187	AGTAGCTTTTCAGGGAGGTG	435
356320	Coding	352	198	AAATGTGCTCCAGTAGCTTT	436
356321	Coding	352	203	TCAGTAAATGTGCTCCAGTA	437
356322	Coding	352	208	CCGTGTCAGTAAATGTGCTC	438
356323	Coding	352	213	GGAGACCGTGTCAGTAAATG	439
356324	Coding	352	218	AGGCTGGAGACCGTGTCAGT	440
356325	Coding	352	223	CCCAGAGGCTGGAGACCGTG	441
356326	Coding	352	228	AGAATCCCAGAGGCTGGAGA	442
356327	Stop Codon	352	274	AGAGGTCTCAAGGCTCAGTA	443
356328	Stop Codon	352	279	AACGTAGAGGTCTCAAGGCT	444
356329	Stop Codon	352	284	TTTGGAACGTAGAGGTCTCA	445
356330	3' UTR	352	289	GCACATTTGGAACGTAGAGG	446
356331	3' UTR	352	294	CACAAGCACATTTGGAACGT	447
356332	3' UTR	352	299	GGACACACAAGCACATTTGG	448
356333	3' UTR	352	304	AGGATGGACACACAAGCACA	449
356334	3' UTR	352	309	CCAGCAGGATGGACACACAA	450
356335	3' UTR	352	314	AGAGGCCAGCAGGATGGACA	451
356336	3' UTR	352	319	GGCCCAGAGGCCAGCAGGAT	452
356337	3' UTR	352	324	ACCCAGGCCCAGAGGCCAGC	453
356338	3' UTR	352	329	GGGCCACCCAGGCCCAGAGG	454
356339	3' UTR	352	353	CTTTCCCTTTCAAACAACCT	455
356340	3' UTR	352	358	CAATACTTTCCCTTTCAAAC	456
356341	3' UTR	352	363	CATGACAATACTTTCCCTTT	457
356342	3' UTR	352	368	GAAAACATGACAATACTTTC	458
356343	3' UTR	352	373	GGGATGAAAACATGACAATA	459
356344	3' UTR	352	396	CATGTTTAGGTGACTTCTGG	460
356345	3' UTR	352	401	GACAGCATGTTTAGGTGACT	461
356346	3' UTR	352	406	TTTAGGACAGCATGTTTAGG	462
356347	3' UTR	352	411	CTTTATTTAGGACAGCATGT	463
356348	3' UTR	352	416	TCCAGCTTTATTTAGGACAG	464

Example 40: Antisense inhibition of hamster apolipoprotein C-III by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap: dose response studies in primary hamster hepatocytes

In a further embodiment, six oligonucleotides targeted to hamster apolipoprotein C-III were selected for additional dose response studies. Primary hamster hepatocytes were treated with 50, 150, and 300 nM of ISIS 352939 (SEQ ID NO: 369), ISIS 352952 (SEQ ID NO: 380), ISIS 352962 (SEQ ID NO:

389), ISIS 352963 (SEQ ID NO: 390), ISIS 352971 (SEQ ID NO: 397), or ISIS 352977 (SEQ ID NO: 403) and mRNA levels were measured 24 hours after oligonucleotide treatment as described in other examples herein. Untreated cells served as the control to which the data were normalized.

Results of these studies are shown in Table 20. Data are averages from three experiments and are expressed as percent inhibition, relative to untreated controls.

Table 20 - Inhibition of apolipoprotein C-III mRNA expression in primary hamster hepatocytes 24 hours after oligonucleotide treatment

		Dose of oligonucleotide		
ISIS #	SEQ ID NO	50 nM	150 nM	300 nM
		% Inhibition		
352939	369	46	64	82
352952	380	59	68	60
352962	389	84	0	22
352963	390	0	0	42
352971	397	0	27	0
352977	403	48	72	56

As shown in Table 20, ISIS 352939 was effective at reducing hamster apolipoprotein C-III mRNA levels in a dose-dependent manner.

Example 41: Antisense oligonucleotides targeted to mouse apolipoprotein C-III

In a further embodiment, additional antisense oligonucleotides targeting mouse apolipoprotein C-III were designed using published sequence information (GenBank accession number L04150.1, incorporated herein as SEQ ID NO: 11). Both target nucleotide position 496 of SEQ ID NO: 11, as does ISIS 167880 (SEQ ID NO: 117), but vary in chemical composition relative to ISIS 167880. ISIS 340995 is 20

nucleotides in length, composed of a central gap region 10 nucleotides in length, wherein the gap contains both 2' deoxynucleotides and 2'-MOE (MOE)nucleotides. The nucleotide composition is shown in Table 21, where 2'-MOE nucleotides are indicated in bold type, and 2' deoxynucleotides are underscored. The gap is flanked on both sides (5' and 3' ends) by 5 nucleotide "wings" composed of 2'-MOE nucleotides. ISIS 340997 (SEQ ID NO: 117) is 20 nucleotides in length and uniformly composed of 2'-MOE nucleotides. Throughout both ISIS 340995 and ISIS 340997, internucleoside (backbone) linkages are phosphorothioate and all cytidines residues are unmodified cytidines.

Table 21 - Antisense oligonucleotides targeted to mouse apolipoprotein C-III

ISISNO	Region	Target SEQ ID NO	Target Site	SEQUENCE	SEQ ID NO
340995	3' UTR	11	496	**TCTTATCCAGCTTTATTAGG**	117
340997	3' UTR	11	496	**TCTTATCCAGCTTTATTAGG**	117